# MODULATION OF HIF1α and HIF2α EXPRESSION

## FIELD OF THE INVENTION

**[0001]** The present invention provides compositions and methods for modulating the expression of HIF1α (HIF1α) and hypoxia-inducible factor 2 alpha (HIF2α). In particular, this invention relates to compounds, particularly oligonucleotide compounds, which, in preferred embodiments, hybridize with nucleic acid molecules encoding HIF1α and HIF2α. Such compounds are shown herein to modulate the expression of HIF1α and HIF2α.

## BACKGROUND OF THE INVENTION

**[0002]** Oxygen homeostasis is an essential cellular and systemic function; hypoxia leads to metabolic demise, but this must be balanced by the risk of oxidative damage to cellular lipids, nucleic acids, and proteins resulting from hyperoxia. As a result, cellular and systemic oxygen concentrations are tightly regulated via response pathways that affect the activity and expression of a multitude of cellular proteins. This balance is disrupted in heart disease, cancer, cerebrovascular disease, and chronic obstructive pulmonary disease (Semenza, *Genes Dev.*, **2000**, *14*, 1983-1991)(Semenza, G., **2001**, *Trends Mol. Med.*, *7*, 345-350. Cells are typically cultured in the laboratory at an ambient oxygen concentration of 21%, but cells in the human body are exposed to much lower oxygen concentrations ranging from 16%

in the lungs to less than 6% in most other organs of the body- often significantly less in tumors. Semenza G., **2001,** *Trends Mol. Med.*, 7, 345-350.

**[0003]** Solid tumor growth depends on a continuous supply of oxygen and nutrients through neovascularization (angiogenesis). Tumors often become hypoxic, often because new blood vessels are aberrant and have poor blood flow. Cancer cells make adaptive changes that allow them to proliferate even at hypoxia. These changes include an increase in glycolysis and an increase in production of angiogenic factors. Hypoxia in tumors is associated with resistance to radio-and chemotherapy, and thus is an indicator of poor survival.

**[0004]** The transcriptional complex, hypoxia inducible factor (HIF), is a key regulator of oxygen homeostasis. Hypoxia induces the expression of genes participating in many cellular and physiological processes, including oxygen transport and iron metabolism, erythropoiesis, angiogenesis, glycolysis and glucose uptake, transcription, metabolism, pH regulation, growth-factor signaling, response to stress and cell adhesion. These gene products participate in either increasing oxygen delivery to hypoxic tissues or activating an alternative metabolic pathway (glycolysis) which does not require oxygen. Hypoxia-induced pathways, in addition to being required for normal cellular processes, can also aid tumor growth by allowing or aiding angiogenesis, immortalization, genetic instability, tissue invasion and metastasis (Harris, *Nat. Rev. Cancer,* **2002**, *2*, 38-47; Maxwell et al., *Curr. Opin. Genet. Dev.*, **2001**, *11*, 293-299).

**[0005]** HIF is a heterodimer composed of an alpha subunit complexed with a beta subunit, both of which are basic helix-loop-helix transcription factors. The beta subunit of HIF is a constitutive nuclear protein. The alpha

subunit is the regulatory subunit specific to the oxygen response pathway, and can be one of three subunits, HIF1α, 2 alpha or 3 alpha (HIF-1α, HIF-2α and HIF-3α, respectively) (Maxwell et al., *Curr. Opin. Genet. Dev.*, **2001**, *11*, 293-299; Safran and Kaelin, *J. Clin. Invest.*, **2003**, *111*, 779-783).

**[0006]** The transcription factor hypoxia-inducible factor 1 (HIF-1) plays an essential role in homeostatic responses to hypoxia by binding to the DNA sequence 5'-TACGTGCT-3' and activating the transcription of dozens of genes *in vivo* under hypoxic conditions (Wang and Semenza, *J. Biol. Chem.*, **1995**, *270*, 1230-1237). These gene products participate in either increasing oxygen delivery to hypoxic tissues or activating an alternative metabolic pathway (glycolysis) which does not require oxygen. This list includes: aldolase C, enolase 1, glucose transporter 1, glucose transporter 3, glyceraldehyde-3-phosphate dehydrogenase, hexokinase 1, hexokinase 2, insulin-like growth factor-2 (IGF-2), IGF binding protein 1, IGF binding protein 3, lactate dehydrogenase A, phosphoglycerate kinase 1, pyruvate kinase M, p21, transforming growth factor B3, ceruloplasmin, erythropoietin, transferrin, transferrin receptor, a1b-adrenergic receptor, adrenomedullin, endothelin-1, heme oxygenase 1, nitric oxide synthase 2, plasminogen activator inhibitor 1, vascular endothelial growth factor (VEGF), VEGF receptor FTL-1, and p35 (Semenza, *Genes Dev.*, **2000**, *14*, 1983-1991). Expression of HIF1α is also sensitive to oxygen concentration: increased levels of protein are detected in cells exposed to 1% oxygen and these decay rapidly upon return of the cells to 20% oxygen (Wang et al., *Proc. Natl. Acad. Sci. U. S. A.*, **1995**, *92*, 5510-5514).

**[0007]** Hypoxia-inducible factor-1 alpha is a heterodimer composed of a 120 kDa alpha subunit complexed with a 91 to 94 kDa beta subunit, both of which contain a

basic helix-loop-helix (Wang and Semenza, *J. Biol. Chem.*, **1995**, *270*, 1230-1237). The gene encoding hypoxia-inducible factor-1 alpha (HIF1α, also called HIF-1 alpha, HIF1A, HIF-1A, HIF1-A, and MOP1) was cloned in 1995 (Wang et al., *Proc. Natl. Acad. Sci. U. S. A.*, **1995**, *92*, 5510-5514). A nucleic acid sequence encoding HIF1α is disclosed and claimed in US Patent 5,882,914, as are expression vectors expressing the recombinant DNA, and host cells containing said vectors (Semenza, **1999**).

**[0008]** HIF1α expression and HIF-1 transcriptional activity are precisely regulated by cellular oxygen concentration. The beta subunit is a constitutive nuclear protein, while the alpha subunit is the regulatory subunit. HIF1α mRNA is expressed at low levels in tissue culture cells, but it is markedly induced by hypoxia or ischemia *in vivo* (Yu et al., *J. Clin. Invest.*, **1999**, *103*, 691-696). HIF1α protein is negatively regulated in non-hypoxic cells by ubiquitination and proteasomal degradation (Huang et al., *Proc. Natl. Acad. Sci. U. S. A.*, **1998**, *95*, 7987-7992). Under hypoxic conditions, the degradation pathway is inhibited, HIF1α protein levels increase dramatically, and the fraction that is ubiquitinated decreases. HIF1α then translocates to the nucleus and dimerizes with a beta subunit (Sutter et al., *Proc. Natl. Acad. Sci. U. S. A.*, **2000**, *97*, 4748-4753).

**[0009]** A natural antisense transcript that is complementary to the 3′ untranslated region of HIF1α mRNA has been discovered and is named "aHIF" (Thrash-Bingham and Tartof, *J. Natl. Cancer Inst.*, **1999**, *91*, 143-151). This is the first case of overexpression of a natural antisense transcript exclusively associated with a specific human malignant disease. aHIF is specifically overexpressed in nonpapillary clear-cell renal carcinoma under both normoxic and hypoxic conditions, but not in papillary renal carcinoma.

Although aHIF is not further induced by hypoxia in nonpapillary disease, it can be induced in lymphocytes where there is a concomitant decrease in HIF1α mRNA.

**[0010]** HIF1α plays an important role in promoting tumor progression and is overexpressed in common human cancers, including breast, colon, lung, and prostate carcinoma. Overexpression of HIFs is sometimes observed in cancers, such as clear cel renal cell carcinoma, even at normoxia. Mutations that inactivate tumor suppressor genes or activate oncogenes have, as one of their consequences, upregulation of HIF1α activity, either through an increase in HIF1α protein expression, HIF1α transcriptional activity, or both (Semenza, *Pediatr. Res.*, **2001**, *49*, 614-617).

**[0011]** Until a tumor establishes a blood supply, the hypoxic conditions limit tumor growth. Subsequent increases in HIF1α activity result in increased expression of target genes such as vascular endothelial growth factor (VEGF). VEGF expression is essential for vascularization and the establishment of angiogenesis in most solid tumors (Iyer et al., *Genes Dev.*, **1998**, *12*, 149-162). A significant association between hypoxia-inducible factor-1 alpha, VEGF overexpression and tumor grade is also seen in human glioblastoma multiforme, the highest grade glioma in which mean patient survival time is less than one year. The rapidly proliferating tumor outgrows its blood supply, resulting in extensive necrosis, and these regions express high levels of HIF1α protein and VEGF mRNA, suggesting a response of the tumor to hypoxia (Zagzag et al., *Cancer*, **2000**, *88*, 2606-2618).

**[0012]** The action of the von Hippel-Landau (VHL) tumor suppressor gene product is implicated in hypoxic gene regulation, in both normal and diseased cells. Individuals with VHL disease are predisposed to renal cysts, clear cell

renal carcinoma, phaeochromocytoma, haemangioblastomas of the central nervous system, angiomas of the retina, islet cell tumors of the pancreas, and endolymphatic sac tumors (Pugh and Ratcliffe, *Semin. Cancer. Biol.*, **2003**, *13*, 83-89). The VHL gene product participates in ubiquitin-mediated proteolysis by acting as the recognition component of the E3-ubiquitin ligase complex involved in the degradation of hypoxia-inducible factor alpha subunits (Cockman et al., *J. Biol. Chem.*, **2000**, *275*, 25733-25741; Ohh et al., *Nat. Cell Biol.*, **2000**, *2*, 423-427). In normal cells, VHL/HIF complexes form and target HIF alpha subunits for destruction (Maxwell et al., *Nature,* **1999**, *399*, 271-275). This is proposed to occur through hydroxylation of the oxygen-dependent domain of HIF2α and subsequent recognition by the VHL gene product, as recognition of a homologous oxygen-dependent domain is the mechanism by which the VHL protein recognizes HIF1α (Maxwell et al., *Nature,* **1999**, *399*, 271-275). HIF2α is in fact hydroxylated by the enzyme prolyl 4-hydroxylases *in vitro* (Hirsila et al., *J. Biol. Chem.*, **2003**).

**[0013]** The p53 tumor suppressor also targets HIF1α for degradation by the proteasome. Loss of p53 activity occurs in the majority of human cancers and indicates that amplification of normal HIF1α levels contributes to the angiogenic switch during tumorigenesis (Ravi et al., *Genes Dev.*, **2000**, *14*, 34-44).

**[0014]** A mouse model of pulmonary hypertension has shown that local inhibition of HIF1α activity in the lung might represent a therapeutic strategy for treating or preventing pulmonary hypertension in at risk individuals. In pulmonary hypertension hypoxia-induced vascular remodeling leads to decreased blood flow, which leads to progressive right heart failure and death. This hypoxia-induced vascular remodeling is markedly impaired in mice that are partially

HIF1α deficient (Yu et al., *J. Clin. Invest.*, **1999**, *103*, 691-696). Decreased vascular density and retarded solid tumor growth is also seen in mouse embryonic stem cells which are deficient for HIF1α (Ryan et al., *Embo J*, **1998**, *17*, 3005-3015).

**[0015]** During hypoxia, cells shift to a glycolytic metabolic mode for their energetic needs and HIF1α is known to upregulate the expression of many glycolytic genes. HIF1α may play a pivotal role in the Warburg effect in tumors, a paradoxical situation in which tumor cells growing under normoxic conditions show elevated glycolytic rates, which enhances tumor growth and expansion. HIF1α mediates the expression of 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3, a gene whose protein product maintains levels of the key regulator of glycolytic flux, fructose-2,6-bisphosphate (Minchenko et al., *J. Biol. Chem.*, **2001**, *14*, 14).

**[0016]** Currently, there are no known therapeutic agents which effectively inhibit the synthesis of HIF1α and to date, investigative strategies aimed at modulating HIF1α function have involved the use of antisense expression vectors and oligonucleotides. These studies have served to define the involvement of HIF1α in disease progression and to identify novel roles of HIF1α *in vivo* including unique roles for HIF1α as a transcription factor under non-hypoxic conditions and as an inhibitor of gene expression.

**[0017]** Gene transfer of an antisense HIF1α plasmid has been shown to enhance the efficacy of cancer immunotherapy. Antisense therapy was shown to slow, but not eradicate, the growth of EL-4 tumors established in mice. In addition, endogenously expression of HIF1α was almost completely inhibited in these tumors. When antisense therapy was combined with T-cell costimulator B7-1 immunotherapy, the

tumors completely and rapidly regressed within 1 week. Furthermore, when these tumor-free mice were rechallenged with EL-4 cells, no tumors emerged, indicating that systemic antitumor immunity had been achieved (Sun et al., *Gene Ther.*, **2001**, *8*, 638-645).

**[0018]** Activation of HIF1α is thought to aggravate heart failure by upregulation of cardiac ET-1, a gene product involved in heart failure and whose inhibition improves the survival rate of rats with heart failure. In a failing heart, a metabolic switch occurs, and HIF1α activates the expression of glycolytic enzymes as compensation for impaired b-oxidation of fatty acid. Another consequence of increased HIF1α activity is that in rat cardiomyocytes, HIF1α was shown to bind to the 5'-promoter region of the ET-1 gene and increase ET-1 expression. *In vitro*, an antisense oligonucleotide targeted to hypoxia-inducible factor-1 alpha largely inhibited the increased gene expression of ET-1, confirming the role of HIF1α in heart failure (Kakinuma et al., *Circulation*, **2001**, *103*, 2387-2394). This antisense oligonucleotide is comprised of 20 nucleotides and targets bases 11 to 31 of the rat HIF1α with GenBank accession number AF_057308 incorporated herein by reference.

**[0019]** Preeclampsia is a disorder of unknown etiology that is the leading cause of fetal and maternal morbidity and mortality. Defective downregulation of HIF1α may play a major role in the pathogenesis of preeclampsia. For most of the first trimester, the human fetus develops under hypoxic conditions but at 10-12 weeks the intervillous space opens, the fetus is exposed to maternal blood and at this stage the trophoblast cells invade the maternal decidua. The switch of the trophoblasts from a proliferative to an invasive phenotype is controlled by cellular oxygen concentration. The proliferative, non-invasive trophoblast phenotype appears

to be maintained by HIF1α mediated expression of TGFbeta3 because treatment of human villous explants with an antisense oligonucleotide against HIF1α or TGF beta 3 induces invasion under hypoxic conditions. In this case the HIF1α antisense oligonucelotide was comprised of phosphorothioate oligonucleotides, 16 nucleotides in length, and targeted to the AUG codon (Caniggia et al., *J. Clin. Invest.*, **2000**, *105*, 577-587.; Caniggia et al., *Placenta*, **2000**, *21 Suppl A*, S25-30).

**[0020]** The human intestinal trefoil factor (ITF) gene product protects the epithelial barrier during episodes of intestinal hypoxia. The ITF gene promoter bears a binding site for hypoxia-inducible factor-1 alpha, and the function of HIF1α as a transcription factor for ITF was confirmed *in vitro*. T84 colonic epithelial cells were treated with a phosphorothioate antisense oligonucleotide, 15 nucleotides in length and targeted to the AUG codon of HIF1α and this resulted in a loss of ITF hypoxia inducibility (Furuta et al., *J. Exp. Med.*, **2001**, *193*, 1027-1034).

**[0021]** Human epidemiological and animal studies have associated inhalation of nickel dusts with an increased incidence of pulmonary fibrosis. Nickel transcriptionally activates plasminogen activator inhibitor (PAI-1), an inhibitor of fibrinolysis, through the HIF1α signaling pathway. This was evidenced by decreases in PAI-1 mRNA levels when human airway epithelial cells were treated with an antisense oligonucleotide directed against HIF1α identical to the one used in the preeclampsia study discussed above. These data may be critical for understanding the pathology of pulmonary fibrosis and other diseases associated with nickel exposure (Andrew et al., *Am J Physiol Lung Cell Mol Physiol*, **2001**, *281*, L607-615).

**[0022]** HIF1α is constitutively expressed in cerebral neurons under normoxic conditions. A second dimerization partner for HIF1α is ARNT2, a cerebral translocator homologous to hypoxia-inducible factor-1 beta. One splice variant of HIF1α found in rat neurons dimerizes with ARNT2 more avidly than it does with HIF1b, and the resulting hypoxia-inducible factor-1 alpha-ARNT2 heterodimer does not recognize the HIF1α binding site of the erythropoietin gene. This suggests that transcription of a different set of genes is controlled by the hypoxia-inducible factor-1 alpha-ARNT2 heterodimer controls in neurons under nonhypoxic conditions than the hypoxia-inducible factor-1 alpha- HIF1α heterodimer controls under hypoxic conditions. This was evidenced by antisense oligonucleotide downregulation of HIF1α expression in which the antisense oligonucleotide consisted of 16 phosphorothioate nucleotides targeted to bases 38 to 54 of the rat hypoxia-inducible factor-1 with GenBank accession number AF_057308 (Drutel et al., *Eur. J. Neurosci.*, **2000**, *12*, 3701-3708).

**[0023]** A role for HIF1α in mediating a down-regulatory pathway was recently discovered using antisense oligonucleotide depletion of hypoxia-inducible factor-1 alpha. The peroxisome proliferator-activated receptors (PPARs) are a nuclear hormone-binding proteins that regulate transcriptional activities. Ligands which bind the PPAR-gamma isoform man amplify or inhibit the expression of inflammation-related gene products and may regulate the duration of inflammatory response. Hypoxia elicits a down-regulation of PPAR-gamma in intestinal epithelial cells which is effected through a binding site for HIF1α on the antisense strand of the PPAR-gamma gene. The expression of PPAR-gamma was upregulated in hypoxic cells when treated with an antisense oligonucleotide targeted to HIF1α identical to the

one used in the preeclampsia study discussed above (Narravula and Colgan, *J. Immunol.*, **2001**, *166*, 7543-7548).

**[0024]** The gene encoding hypoxia-inducible factor 2 alpha (HIF2α; also called HIF-2 alpha, endothelial PAS domain protein 1, EPAS1, MOP2, hypoxia-inducible factor 2, HIF-related factor, HRF, HIF1 alpha-like factor, HLF) was initially identified as a transcription factor expressed in endothelial cells (Ema et al., *Proc. Natl. Acad. Sci. U. S. A.*, **1997**, *94*, 4273-4278; Flamme et al., *Mech. Dev.*, **1997**, *63*, 51-60; Hogenesch et al., *J. Biol. Chem.*, **1997**, *272*, 8581-8593; Tian et al., *Genes Dev.*, **1997**, *11*, 72-82). A nucleic acid sequence encoding human HIF2α is disclosed and claimed in US Patent 5,695,963 (McKnight et al., **1997**).

**[0025]** HIF2α mRNA is primarily expressed in highly vascularized adult tissues, such as lung, heart and liver, and in the placenta and endothelial cells of the embryonic and adult mouse (Hogenesch et al., *J. Biol. Chem.*, **1997**, *272*, 8581-8593). Comparison of normal human tissues and cancers reveals that HIF2α protein is not detectable in normal tissue, but is easily visualized in malignant tissues (Talks et al., *Am. J. Pathol.*, **2000**, *157*, 411-421). The requirement for expression of HIF2α in development is demonstrated by the abnormalities observed in HIF2α gene deficient mouse embyros, which include the disruption of catecholamine homeostasis and lack of protection against heart failure observed (Tian et al., *Genes Dev.*, **1998**, *12*, 3320-3324). Targeted disruption of the HIF2α gene and generation of embryos deficient for HIF2α is disclosed in the PCT publication WO 02/086497 (Compernolle et al., **2002**). This publication also discloses antisense oligodeoxyribonucleotides for use in inhibiting HIF2α expression targeted to the translation initiation codon of HIF2α (Compernolle et al., **2002**).

**[0026]** HIF2α expression and HIF transcriptional activity are precisely regulated by cellular oxygen concentration. Whereas changes in oxygen levels do not affect HIF1-beta protein levels, the abundance of the alpha subunits is markedly increased upon exposure of cells to hypoxia, primarily due to stabilization of the alpha subunit protein (Safran and Kaelin, *J. Clin. Invest.*, **2003**, *111*, 779-783). HIF2α mRNA and protein is expressed at low levels in tissue culture cells, but protein expression is markedly induced by exposure to 1% oxygen, a hypoxic state (Wiesener et al., *Blood,* **1998**, *92*, 2260-2268). The hypoxia-inducible factor 2 alpha/hypoxia-inducible factor 1 beta heterodimer protein binds to the hypoxic response element, which contains the core recognition sequence 5'-TACGTG-3' and is found in the cis-regulatory regions of hypoxia-regulated genes (Ema et al., *Proc. Natl. Acad. Sci. U. S. A.*, **1997**, *94*, 4273-4278; Hogenesch et al., *J. Biol. Chem.*, **1997**, *272*, 8581-8593). Binding of the heterodimer to the HRE induces gene expression. Upon return to normoxic conditions, HIF2α protein is rapidly degraded (Wiesener et al., *Blood,* **1998**, *92*, 2260-2268).

**[0027]** The mitogen-activated protein kinase (MAPK) pathway is critical for HIF2α activation. Inhibition of a dual specificity protein kinase that directly phosphorylates MAPK prevents HIF2α trans-activation during hypoxia (Conrad 1999; Conrad, 2001). However, the inhibitor does not prevent HIF2α phosphorylation, thus, while the MAPK pathway regulates the activity of hypoxia-inducible factor 2 alpha, it does not directly phosphorylate the protein (Conrad et al., *Comp. Biochem. Physiol. B. Biochem. Mol Biol.*, **2001**, *128*, 187-204; Conrad et al., *J. Biol. Chem.*, **1999**, *274*, 33709-33713). The Src family kinase pathway is also implicated in regulation of hypoxia-inducible factor 2 alpha. A specific inhibitor of

the Src family of kinases abolishes the hypoxia-induced expression of HIF2α mRNA in human lung adenocarcinoma cells (Sato et al., *Am. J. Respir. Cell Mol. Biol.*, **2002**, *26*, 127-134).

**[0028]** The maintenance of oxygen homeostasis, in addition to being required in physiological development, is also required in tumor growth. Tumor cells experience hypoxia because blood circulates poorly through the aberrant blood vessel that tumors establish. Although hypoxia is toxic to cancer cells, they survive as a result of genetic and adaptive changes that allow them to thrive in a hypoxic environment. One such adaptation is an increase in the expression of the angiogenic growth factor named vascular endothelial growth factor (VEGF). VEGF is a key angiogenic factor secreted by cancer cells, as well as normal cells, in response to hypoxia (Harris, *Nat. Rev. Cancer*, **2002**, *2*, 38-47; Maxwell et al., *Curr. Opin. Genet. Dev.*, **2001**, *11*, 293-299).

**[0029]** Hemangioblastomas, the most frequent manifestation of VHL gene mutations, exhibit overexpression of VEGF mRNA in their associated stromal cells. The VEGF mRNA overexpression is highly correlated with elevated expression of HIF2α mRNA. This finding suggests a relationship between loss of function of the VHL gene, and transcriptional activation of the VEGF gene, possibly through HIF2α activity in VEGF-dependent vascular growth (Flamme et al., *Am. J. Pathol.*, **1998**, *153*, 25-29).

**[0030]** The tumor suppressive activity of the VHL gene product can be overridden by the activation of HIF target genes in human renal carcinoma cells *in vivo*. VHL gene product mutants lose the ability to target HIF for ubiquitin-mediated destruction, suggesting that down regulation of HIF and VHL tumor suppressor function are intimately linked

(Kondo et al., *Cancer Cell*, **2002**, *1*, 237-246). In contrast to human renal cell carcinoma, the product of the tuberous sclerosis complex-2 (Tsc-2) gene, product rather than VHL gene, is the primary target for rodent renal cell carcinoma (Liu et al., *Cancer Res.*, **2003**, *63*, 2675-2680). Rat RCC cells lacking Tsc-2 function exhibit stabilization of HIF2α protein and upregulation of VEGF, and were highly vascularized (Liu et al., *Cancer Res.*, **2003**, *63*, 2675-2680).

**[0031]** A link between elevated HIF2α activity and angiogenesis has also been demonstrated by experiments that show how HIF activity regulates VEGF expression. Normal human kidney cells typically have low levels of hypoxia-inducible factor 2 alpha, but upon introduction of a vector encoding HIF2α into these cells, VEGF mRNA and protein levels increase significantly (Xia et al., *Cancer*, **2001**, *91*, 1429-1436). When HIF2α was inhibited, VEGF expression was significantly decreased, thus demonstrating a direct link between HIF2α activity and VEGF expression (Xia et al., *Cancer*, **2001**, *91*, 1429-1436). Similarly, a dose-dependent increase in VEGF mRNA is observed when human umbulical vein cells are transduced with a virus encoding HIF2α (Maemura et al., *J. Biol. Chem.*, **1999**, *274*, 31565-31570). Expression of a mutated HIF2α that lacks a transactivation domain inhibits the induction of VEGF mRNA during hypoxia, a finding that further suggests that HIF2α is an important regulator of VEGF expression (Maemura et al., *J. Biol. Chem.*, **1999**, *274*, 31565-31570).

**[0032]** A correlation between HIF activity and VEGF expression is also observed in malignant cells and tissues. HIF2α can be readily detected in renal cell carcinoma (RCC) cell lines in the absence of a vector encoding HIF2α (Xia et al., *Cancer*, **2001**, *91*, 1429-1436). Significant increases in HIF2α and VEGF mRNA in renal cell carcinoma tissue samples,

compared to normal tissue, suggest that abnormal activation of HIF2α may be involved in the angiogenesis of RCC (Xia et al., *Cancer,* **2001**, *91*, 1429-1436).

**[0033]** In addition to RCC, the expression of HIF2α in other malignancies has also been reported. HIF2α is expressed at the levels of mRNA and protein in human bladder cancers, especially in those with an invasive phenotype (Xia et al., *Urology,* **2002**, *59*, 774-778). Another example of overexpression of HIF2α is seen in squamous cell head-and-neck cancer (SCHNC). Higher levels of HIF2α were associated with locally aggressive behavior of SCHNC, as well as intensification of angiogenesis (Koukourakis et al., *Int. J. Radiat. Oncol. Biol. Phys.*, **2002**, *53*, 1192-1202). These findings also demonstrated a link between overexpression of HIF2α and resistance to chemotherapy. Yet another correlation between overexpression of HIF2α and cancer is seen in malignant pheochromocytomas, which exhibit a higher level of HIF2α and an induced VEGF pathway, when compared to benign counterparts (Favier et al., *Am. J. Pathol.*, **2002**, *161*, 1235-1246). HIF2α overexpression is also a common event in non-small-cell lung cancer (NSCLC) and is related to the up-regulation of multiple angiogenic factors and overexpression of angiogenic receptors by cancer cells. HIF2α overexpression in NSCLC is an indicator of poor prognosis (Giatromanolaki et al., *Br. J. Cancer,* **2001**, *85*, 881-890). Taken together, these studies demonstrate that elevated HIF2α confers aggressive tumor behavior, and that targeting the HIF pathway may aid the treatment of several different types of cancers.

**[0034]** Overexpression of HIF2α has also been observed in several cancer cell lines in addition to RCC cell lines. Elevated levels of HIF2α mRNA and protein are seen in human lung adenocarcinoma cells, and exposure of these cells to

hypoxia further increases HIF2α expression (Sato et al., *Am. J. Respir. Cell Mol. Biol.*, **2002**, *26*, 127-134). Furthermore, the hypoxia response element plays a role in constitutively upregulating an isoform of VEGF in cancer cell lines under normoxic conditions. The HRE located within a cell type-specific enhancer element in glioblastoma cells participates in the up-regulation of VEGF expression through enhanced binding of HIF2α to the HRE (Liang et al., *J. Biol. Chem.*, **2002**, *277*, 20087-20094). A truncated version of HIF2α that can bind to hypoxia-inducible factor 1 beta, but not to the HRE, was unable to transactivate the VEGF promoter (Liang et al., *J. Biol. Chem.*, **2002**, *277*, 20087-20094). This further demonstrates the capability of cancer cells to combat hypoxic conditions by enhancing expression of factors required for vascularization and angiogenesis.

**[0035]** Short interfering RNAs (siRNAs) have been used to specifically inhibit the expression of HIF1α and HIF2α in human breast and renal carcinoma cell lines and in a human endothelial cell line. SiRNA duplexes with dTdT overhangs at both ends were designed to target nucleotides 1521-1541 and 1510-1530 of the HIF1α mRNA squence (NM001530) and nucleotides 1260-1280 and 328-348 of the HIF2α sequence (NM001430). It was found that in the breast carcinoma and endothelial cell lines, gene expression and cell migration patterns were critically dependent on HIF1α but not hypoxia-inducible factor-2 alpha, but critically dependent on HIF2α in the renal carcinoma cells. Sowter et al., **2003**, *Cancer Res.*, *63*, 6130-6134.

**[0036]** Defective downregulation of HIF2α may play a major role in the pathogenesis of preeclampsia. HIF2α protein levels are increased during early development, as expected in a hypoxic environment, and then decrease significantly with gestational age (Rajakumar and Conrad,

*Biol. Reprod.*, **2000**, *63*, 559-569). However, HIF2α protein expression is significantly increased in preeclamptic relative to normal term placentas (Rajakumar et al., *Biol. Reprod.*, **2001**, *64*, 499-506). This result suggests that failure to down-regulate HIF2α protein expression during early pregnancy could prevent the switch of the trophoblast to an invasive phenotype and ultimately lead to preeclampsia (Rajakumar et al., *Biol. Reprod.*, **2001**, *64*, 499-506).

**[0037]** Overexpression of hypoxia-inducible factor 2 alpha, as well as hypoxia-inducible factor 1, has been observed in the inflammatory bowel diseases Crohn's disease and ulcerative colitis (Giatromanolaki et al., *J. Clin. Pathol.*, **2003**, *56*, 209-213). However, VEGF expression was weak in ulcerative colitis samples, and absent in Crohn's disease samples. The discordant expression of VEGF and HIF2α may lead to a reduced ability of a tissue to produce or respond to VEGF, which may in turn lead to reduced endothelial and epithelial cell viability (Giatromanolaki et al., *J. Clin. Pathol.*, **2003**, *56*, 209-213).

**[0038]** In addition to participating in adaptive changes in response to hypoxia, HIF2α may also function in an inflammatory response in cardiac myocytes. In cultured cardiac myocytes, interleukin-1 beta (IL-1beta) significantly increased both HIF2α mRNA and protein levels (Tanaka et al., *J. Mol. Cell Cardiol.*, **2002**, *34*, 739-748). Transduction of cardiac myocytes with adenovirus expressing HIF2α dramatically increased the levels of adrenomedullin (AM) mRNA, which is also upregulated by IL-1beta (Tanaka et al., *J. Mol. Cell Cardiol.*, **2002**, *34*, 739-748). Since IL-1 beta has been implicated in the pathogenesis of heart failure, and AM is known to improve cardiac function during heart failure, these results suggest that HIF2α plays a role in the

adaptation of the cardiac myocytes during heart failure (Tanaka et al., *J. Mol. Cell Cardiol.*, **2002**, *34*, 739-748).

**[0039]** Disclosed and claimed in the PCT publication WO 00/09657 is a method of inhibiting angiogenesis in a mammal through administration of a compound which inhibits the binding of human HIF2α protein to the DNA regulatory element of an angiogenic factor, wherein the compound can be an antisense nucleic acid molecule complementary to all or part of the mRNA encoding human HIF2α (Lee et al., **2000**). This publication also discloses a nucleic acid encoding human hypoxia-inducible factor 2 alpha.

**[0040]** The PCT publication WO 01/62965 discloses and claims a differential screening method for identifying a genetic element involved in a cellular process, which method includes introducing HIF2α into cells (Kingsman, **2001**). This publication also discloses the development of HIF2α agonists or antagonists.

**[0041]** The PCT publication WO 02/34291 claims methods and reagents, including the use of antisense oligonucleotides, for the inhibition of human HIF1α transcription (Colgan, **2002**). This publication also discloses a nucleic acid encoding human hypoxia-inducible factor 2 alpha.

**[0042]** US patent 6,395,548 claims a nucleic acid encoding a deletion mutant of human HIF2α and the use of this deletion mutant as a method of inhibiting expression of an angiogenic factor *in vitro*. This patent also discloses a nucleic acid encoding human hypoxia-inducible factor 2 alpha, as well as nucleic acids complementary to all or part of the human HIF2α cDNA for use in antisense treatment to inhibit the expression of HIF2α (Lee et al., **2002**).

**[0043]** US patent 6,432,927 discloses nucleic acid sequences, including sense and antisense oligonucleotides,

which are derived from an HIF2α and incorporated into recombinant nucleic acid molecules for the purpose of sustaining HIF2α expression in cells (Gregory and Vincent, **2002**).

**[0044]** The nucleic acid sequence encoding a human HIF2α and insertion of this sequence into a viral expression vector, for the purpose of driving human HIF2α expression in mammalian cells, is disclosed in the PCT publication WO 02/068466 (White et al., **2002**).

**[0045]** The PCT publication WO 02/094862 discloses a method for introducing into a muscle cell a nucleic acid sequence encoding hypoxia-inducible factor 2 alpha, for the purpose of overexpressing HIF2α and stimulating angiogenesis or metabolic activity (Guy, **2002**).

**[0046]** Disclosed and claimed in the US pre-grant publication 2003/0045686 is a nucleic acid encoding human hypoxia-inducible factor 2 alpha, and a method of delivering a therapeutically effective amount of this nucleic acid to a subject for the purpose of reducing or preventing hypoxia (Kaelin Jr. and Ivan, **2003**). This publication also discloses and claims human HIF muteins, including HIF2α mutein, which are designed to be more stable and/or resistant to degradation.

**[0047]** As a consequence of HIF2α involvement in many diseases, there remains a long felt need for additional agents capable of effectively regulating HIF2α function. As such, inhibition is especially important in the treatment of cancer, given that the upregulation of expression of HIF2α is associated with so many different types of cancer.

**[0048]** As a consequence of HIF1α and HIF2α involvement in many diseases, there remains a long felt need for additional agents capable of effectively inhibiting HIF1α and HIF2α function.

**[0049]** Antisense technology is emerging as an effective means for reducing the expression of specific gene products and may therefore prove to be uniquely useful in a number of therapeutic, diagnostic, and research applications for the modulation of HIF1α and HIF2α expression.

**[0050]** The present invention provides compositions and methods for modulating HIF1α and HIF2α expression. In particular antisense compositions for modulating HIF1α and/or HIF2α expression are believed to be useful in treatment of abnormal proliferative conditions associated with HIF1α and/or HIF2α. Examples of abnormal proliferative conditions are hyperproliferative disorders such as cancers, tumors, hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis, atherosclerosis and smooth muscle cell proliferation in the blood vessels, such as stenosis or restenosis following antioplasty. It is presently believed that inhibition of both HIF1α and HIF2α may be a particularly useful approach to treatment of such disorders.

## SUMMARY OF THE INVENTION

**[0051]** The present invention is directed to compounds, especially nucleic acid and nucleic acid-like oligomers, which are targeted to a nucleic acid encoding HIF1α and/or HIF2α, and which modulate the expression of HIF1α and/or HIF2α. Pharmaceutical and other compositions comprising the compounds of the invention are also provided. Further provided are methods of screening for modulators of HIF1α and/or HIF2α and methods of modulating the expression of HIF1α and/or HIF2α in cells, tissues or animals comprising contacting said cells, tissues or animals with one or more of the compounds or compositions of the invention. Methods of treating an animal, particularly a human, suspected of having

or being prone to a disease or condition associated with expression of HIF1α and/or HIF2α are also set forth herein. Such methods comprise administering a therapeutically or prophylactically effective amount of one or more of the compounds or compositions of the invention to the person in need of treatment.

## DETAILED DESCRIPTION OF THE INVENTION

### A. Overview of the Invention

**[0052]** The present invention employs compounds, preferably oligonucleotides and similar species for use in modulating the function or effect of nucleic acid molecules encoding HIF1α or HIF2α. This is accomplished by providing oligonucleotides which specifically hybridize with one or more nucleic acid molecules encoding HIF1α or HIF2α. Thus "target nucleic acid" refers to a nucleic acid molecule encoding HIF1α or HIF2α. As used herein, the term "nucleic acid molecule encoding HIF1α" has been used for convenience to encompass DNA encoding HIF1α, RNA (including pre-mRNA and mRNA or portions thereof) transcribed from such DNA, and also cDNA derived from such RNA. Similarly, the term "nucleic acid molecule encoding HIF2α" has been used for convenience to encompass DNA encoding HIF2α, RNA (including pre-mRNA and mRNA or portions thereof) transcribed from such DNA, and also cDNA derived from such RNA. The hybridization of a compound of this invention with its target nucleic acid is generally referred to as "antisense". Consequently, the preferred mechanism believed to be included in the practice of some preferred embodiments of the invention is referred to herein as "antisense inhibition." Such antisense inhibition is typically based upon hydrogen bonding-based hybridization of oligonucleotide strands or segments such that at least one strand or segment is cleaved, degraded, or otherwise rendered

inoperable. In this regard, it is presently preferred to target specific nucleic acid molecules and their functions for such antisense inhibition.

**[0053]** The functions of DNA to be interfered with can include replication and transcription. Replication and transcription, for example, can be from an endogenous cellular template, a vector, a plasmid construct or otherwise. The functions of RNA to be interfered with can include functions such as translocation of the RNA to a site of protein translation, translocation of the RNA to sites within the cell which are distant from the site of RNA synthesis, translation of protein from the RNA, splicing of the RNA to yield one or more RNA species, and catalytic activity or complex formation involving the RNA which may be engaged in or facilitated by the RNA. One preferred result of such interference with target nucleic acid function is modulation of the expression of HIF1α or HIF2α. In the context of the present invention, "modulation" and "modulation of expression" mean either an increase (stimulation) or a decrease (inhibition) in the amount or levels of a nucleic acid molecule encoding the gene, e.g., DNA or RNA. Inhibition is often the preferred form of modulation of expression and mRNA is often a preferred target nucleic acid.

**[0054]** In the context of this invention, "hybridization" means the pairing of complementary strands of oligomeric compounds. In the present invention, the preferred mechanism of pairing involves hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleoside or nucleotide bases (nucleobases) of the strands of oligomeric compounds. For example, adenine and thymine are complementary nucleobases which pair through the formation of

hydrogen bonds. Hybridization can occur under varying circumstances.

**[0055]** An antisense compound is specifically hybridizable when binding of the compound to the target nucleic acid interferes with the normal function of the target nucleic acid to cause a loss of activity, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target nucleic acid sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and under conditions in which assays are performed in the case of *in vitro* assays.

**[0056]** In the present invention the phrase "stringent hybridization conditions" or "stringent conditions" refers to conditions under which a compound of the invention will hybridize to its target sequence, but to a minimal number of other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances and in the context of this invention, "stringent conditions" under which oligomeric compounds hybridize to a target sequence are determined by the nature and composition of the oligomeric compounds and the assays in which they are being investigated.

**[0057]** "Complementary," as used herein, refers to the capacity for precise pairing between two nucleobases of an oligomeric compound. For example, if a nucleobase at a certain position of an oligonucleotide (an oligomeric compound), is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, said target nucleic acid being a DNA, RNA, or oligonucleotide molecule, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be a complementary position. The oligonucleotide and the

further DNA, RNA, or oligonucleotide molecule are complementary to each other when a sufficient number of complementary positions in each molecule are occupied by nucleobases which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of precise pairing or complementarity over a sufficient number of nucleobases such that stable and specific binding occurs between the oligonucleotide and a target nucleic acid.

**[0058]** It is understood in the art that the sequence of an antisense compound need not be 100% complementary to that of its target nucleic acid to be specifically hybridizable. Moreover, an oligonucleotide may hybridize over one or more segments such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure or hairpin structure). It is preferred that the antisense compounds of the present invention comprise at least 70% sequence complementarity to a target region within the target nucleic acid, more preferably that they comprise 90% sequence complementarity and even more preferably comprise 95% sequence complementarity to the target region within the target nucleic acid sequence to which they are targeted. For example, an antisense compound in which 18 of 20 nucleobases of the antisense compound are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In this example, the remaining noncomplementary nucleobases may be clustered or interspersed with complementary nucleobases and need not be contiguous to each other or to complementary nucleobases. As such, an antisense compound which is 18 nucleobases in length having 4 (four) noncomplementary nucleobases which are flanked by two regions of complete complementarity with the target nucleic acid would have 77.8% overall complementarity

with the target nucleic acid and would thus fall within the scope of the present invention. Percent complementarity of an antisense compound with a region of a target nucleic acid can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs known in the art (Altschul et al., *J. Mol. Biol.*, **1990**, 215, 403-410; Zhang and Madden, *Genome Res.*, **1997**, 7, 649-656).

**B. Compounds of the Invention**

**[0059]** According to the present invention, compounds include antisense oligomeric compounds, antisense oligonucleotides, ribozymes, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and other oligomeric compounds which hybridize to at least a portion of the target nucleic acid. As such, these compounds may be introduced in the form of single-stranded, double-stranded, circular or hairpin oligomeric compounds and may contain structural elements such as internal or terminal bulges or loops. Once introduced to a system, the compounds of the invention may elicit the action of one or more enzymes or structural proteins to effect modification of the target nucleic acid.

**[0060]** One non-limiting example of such an enzyme is RNAse H, a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. It is known in the art that single-stranded antisense compounds which are "DNA-like" elicit RNAse H. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide-mediated inhibition of gene expression. Similar roles have been postulated for other ribonucleases such as those in the RNase III and ribonuclease L family of enzymes.

**[0061]** While the preferred form of antisense compound is a single-stranded antisense oligonucleotide, in many species the introduction of double-stranded structures, such as double-stranded RNA (dsRNA) molecules, has been shown to induce potent and specific antisense-mediated reduction of the function of a gene or its associated gene products. This phenomenon occurs in both plants and animals and is believed to have an evolutionary connection to viral defense and transposon silencing.

**[0062]** The first evidence that dsRNA could lead to gene silencing in animals came in 1995 from work in the nematode, *Caenorhabditis elegans* (Guo and Kempheus, *Cell*, **1995**, 81, 611-620). Montgomery et al. have shown that the primary interference effects of dsRNA are posttranscriptional (Montgomery et al., *Proc. Natl. Acad. Sci. USA*, **1998**, *95*, 15502-15507). The posttranscriptional antisense mechanism defined in *Caenorhabditis elegans* resulting from exposure to double-stranded RNA (dsRNA) has since been designated RNA interference (RNAi). This term has been generalized to mean antisense-mediated gene silencing involving the introduction of dsRNA leading to the sequence-specific reduction of endogenous targeted mRNA levels (Fire et al., *Nature*, **1998**, 391, 806-811). Recently, it has been shown that it is, in fact, the single-stranded RNA oligomers of antisense polarity of the dsRNAs which are the potent inducers of RNAi (Tijsterman et al., *Science*, **2002**, *295*, 694-697).

**[0063]** The oligonucleotides of the present invention also include variants in which a different base is present at one or more of the nucleotide positions in the oligonucleotide. For example, if the first nucleotide is an adenosine, variants may be produced which contain thymidine, guanosine or cytidine at this position. This may be done at any of the positions of the oligonucleotide. These

oligonucleotides are then tested using the methods described herein to determine their ability to inhibit expression of HIF2α mRNA.

**[0064]** In the context of this invention, the term "oligomeric compound" refers to a polymer or oligomer comprising a plurality of monomeric units. In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics, chimeras, analogs and homologs thereof. This term includes oligonucleotides composed of naturally occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for a target nucleic acid and increased stability in the presence of nucleases.

**[0065]** While oligonucleotides are a preferred form of the compounds of this invention, the present invention comprehends other families of compounds as well, including but not limited to oligonucleotide analogs and mimetics such as those described herein.

**[0066]** The compounds in accordance with this invention preferably comprise from about 8 to about 80 nucleobases (i.e. from about 8 to about 80 linked nucleosides). One of ordinary skill in the art will appreciate that the invention embodies compounds of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70,

71, 72, 73, 74, 75, 76, 77, 78, 79, or 80 nucleobases in length.

**[0067]** In one preferred embodiment, the compounds of the invention are 12 to 50 nucleobases in length. One having ordinary skill in the art will appreciate that this embodies compounds of 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleobases in length.

**[0068]** In another preferred embodiment, the compounds of the invention are 15 to 30 nucleobases in length. One having ordinary skill in the art will appreciate that this embodies compounds of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length.

**[0069]** Particularly preferred compounds are oligonucleotides from about 12 to about 50 nucleobases, even more preferably those comprising from about 15 to about 30 nucleobases.

**[0070]** Antisense compounds 8-80 nucleobases in length comprising a stretch of at least eight (8) consecutive nucleobases selected from within the illustrative antisense compounds are considered to be suitable antisense compounds as well.

**[0071]** Exemplary preferred antisense compounds include oligonucleotide sequences that comprise at least the 8 consecutive nucleobases from the 5'-terminus of one of the illustrative preferred antisense compounds (the remaining nucleobases being a consecutive stretch of the same oligonucleotide beginning immediately upstream of the 5'-terminus of the antisense compound which is specifically hybridizable to the target nucleic acid and continuing until the oligonucleotide contains about 8 to about 80 nucleobases). Similarly preferred antisense compounds are

represented by oligonucleotide sequences that comprise at least the 8 consecutive nucleobases from the 3'-terminus of one of the illustrative preferred antisense compounds (the remaining nucleobases being a consecutive stretch of the same oligonucleotide beginning immediately downstream of the 3'-terminus of the antisense compound which is specifically hybridizable to the target nucleic acid and continuing until the oligonucleotide contains about 8 to about 80 nucleobases). One having skill in the art armed with the preferred antisense compounds illustrated herein will be able, without undue experimentation, to identify further preferred antisense compounds.

**C. Targets of the Invention**

**[0072]** "Targeting" an antisense compound to a particular nucleic acid molecule, in the context of this invention, can be a multistep process. The process usually begins with the identification of a target nucleic acid whose function is to be modulated. This target nucleic acid may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target nucleic acid encodes HIF1α or HIF2α.

**[0073]** The targeting process usually also includes determination of at least one target region, segment, or site within the target nucleic acid for the antisense interaction to occur such that the desired effect, e.g., modulation of expression, will result. Within the context of the present invention, the term "region" is defined as a portion of the target nucleic acid having at least one identifiable structure, function, or characteristic. Within regions of target nucleic acids are segments. "Segments" are defined as

smaller or sub-portions of regions within a target nucleic acid. "Sites," as used in the present invention, are defined as positions within a target nucleic acid.

**[0074]** Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon". A minority of genes have a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function *in vivo*. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (in prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used *in vivo* to initiate translation of an mRNA transcribed from a gene encoding HIF1α or HIF2α, regardless of the sequence(s) of such codons. It is also known in the art that a translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively).

**[0075]** The terms "start codon region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. Similarly, the

terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon. Consequently, the "start codon region" (or "translation initiation codon region") and the "stop codon region" (or "translation termination codon region") are all regions which may be targeted effectively with the antisense compounds of the present invention.

**[0076]** The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Within the context of the present invention, a preferred region is the intragenic region encompassing the translation initiation or termination codon of the open reading frame (ORF) of a gene.

**[0077]** Other target regions include the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA (or corresponding nucleotides on the gene), and the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA (or corresponding nucleotides on the gene). The 5' cap site of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as well as the first 50

nucleotides adjacent to the cap site. It is also preferred to target the 5' cap region.

**[0078]** Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," which are excised from a transcript before it is translated. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. Targeting splice sites, i.e., intron-exon junctions or exon-intron junctions, may also be particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular splice product is implicated in disease. Aberrant fusion junctions due to rearrangements or deletions are also preferred target sites. mRNA transcripts produced via the process of splicing of two (or more) mRNAs from different gene sources are known as "fusion transcripts". It is also known that introns can be effectively targeted using antisense compounds targeted to, for example, DNA or pre-mRNA.

**[0079]** It is also known in the art that alternative RNA transcripts can be produced from the same genomic region of DNA. These alternative transcripts are generally known as "variants". More specifically, "pre-mRNA variants" are transcripts produced from the same genomic DNA that differ from other transcripts produced from the same genomic DNA in either their start or stop position and contain both intronic and exonic sequence.

**[0080]** Upon excision of one or more exon or intron regions, or portions thereof during splicing, pre-mRNA variants produce smaller "mRNA variants". Consequently, mRNA variants are processed pre-mRNA variants and each unique pre-mRNA variant must always produce a unique mRNA variant as a result of splicing. These mRNA variants are also known as

"alternative splice variants". If no splicing of the pre-mRNA variant occurs then the pre-mRNA variant is identical to the mRNA variant.

**[0081]** It is also known in the art that variants can be produced through the use of alternative signals to start or stop transcription and that pre-mRNAs and mRNAs can possess more that one start codon or stop codon. Variants that originate from a pre-mRNA or mRNA that use alternative start codons are known as "alternative start variants" of that pre-mRNA or mRNA. Those transcripts that use an alternative stop codon are known as "alternative stop variants" of that pre-mRNA or mRNA. One specific type of alternative stop variant is the "polyA variant" in which the multiple transcripts produced result from the alternative selection of one of the "polyA stop signals" by the transcription machinery, thereby producing transcripts that terminate at unique polyA sites. Within the context of the invention, the types of variants described herein are also preferred target nucleic acids.

**[0082]** The locations on the target nucleic acid to which the preferred antisense compounds hybridize are hereinbelow referred to as "preferred target segments." As used herein the term "preferred target segment" is defined as at least an 8-nucleobase portion of a target region to which an active antisense compound is targeted. While not wishing to be bound by theory, it is presently believed that these target segments represent portions of the target nucleic acid which are accessible for hybridization.

**[0083]** While the specific sequences of certain preferred target segments are set forth herein, one of skill in the art will recognize that these serve to illustrate and describe particular embodiments within the scope of the

present invention. Additional preferred target segments may be identified by one having ordinary skill.

**[0084]** Target segments 8-80 nucleobases in length comprising a stretch of at least eight (8) consecutive nucleobases selected from within the illustrative preferred target segments are considered to be suitable for targeting as well.

**[0085]** Target segments can include DNA or RNA sequences that comprise at least the 8 consecutive nucleobases from the 5'-terminus of one of the illustrative preferred target segments (the remaining nucleobases being a consecutive stretch of the same DNA or RNA beginning immediately upstream of the 5'-terminus of the target segment and continuing until the DNA or RNA contains about 8 to about 80 nucleobases). Similarly preferred target segments are represented by DNA or RNA sequences that comprise at least the 8 consecutive nucleobases from the 3'-terminus of one of the illustrative preferred target segments (the remaining nucleobases being a consecutive stretch of the same DNA or RNA beginning immediately downstream of the 3'-terminus of the target segment and continuing until the DNA or RNA contains about 8 to about 80 nucleobases). One having skill in the art armed with the preferred target segments illustrated herein will be able, without undue experimentation, to identify further preferred target segments.

**[0086]** Once one or more target regions, segments or sites have been identified, antisense compounds are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired effect.

**D. Screening and Target Validation**

**[0087]** In a further embodiment, the "preferred target segments" identified herein may be employed in a screen for additional compounds that modulate the expression of HIF1α or

HIF2α. "Modulators" are those compounds that decrease or increase the expression of a nucleic acid molecule encoding HIF1α or HIF2α and which comprise at least an 8-nucleobase portion which is complementary to a preferred target segment. The screening method comprises the steps of contacting a preferred target segment of a nucleic acid molecule encoding HIF1α or HIF2α with one or more candidate modulators, and selecting for one or more candidate modulators which decrease or increase the expression of a nucleic acid molecule encoding HIF1α or HIF2α. Once it is shown that the candidate modulator or modulators are capable of modulating (e.g. either decreasing or increasing) the expression of a nucleic acid molecule encoding HIF1α or HIF2α, the modulator may then be employed in further investigative studies of the function of HIF1α or HIF2α, or for use as a research, diagnostic, or therapeutic agent in accordance with the present invention.

**[0088]** The preferred target segments of the present invention may be also be combined with their respective complementary antisense compounds of the present invention to form stabilized double-stranded (duplexed) oligonucleotides.

**[0089]** Such double stranded oligonucleotide moieties have been shown in the art to modulate target expression and regulate translation as well as RNA processsing via an antisense mechanism. Moreover, the double-stranded moieties may be subject to chemical modifications (Fire et al., *Nature*, **1998**, *391*, 806-811; Timmons and Fire, *Nature* **1998**, *395*, 854; Timmons et al., *Gene*, **2001**, *263*, 103-112; Tabara et al., *Science*, **1998**, 282, 430-431; Montgomery et al., *Proc. Natl. Acad. Sci. USA*, **1998**, *95*, 15502-15507; Tuschl et al., *Genes Dev.*, **1999**, *13*, 3191-3197; Elbashir et al., *Nature*, **2001**, *411*, 494-498; Elbashir et al., *Genes Dev.* **2001**, *15*, 188-200). For example, such double-stranded moieties have been shown to inhibit the target by the classical

hybridization of antisense strand of the duplex to the target, thereby triggering enzymatic degradation of the target (Tijsterman et al., *Science*, **2002**, *295*, 694-697).

**[0090]** The compounds of the present invention can also be applied in the areas of drug discovery and target validation. The present invention comprehends the use of the compounds and preferred target segments identified herein in drug discovery efforts to elucidate relationships that exist between HIF1α or HIF2α and a disease state, phenotype, or condition. These methods include detecting or modulating HIF1α or HIF2α comprising contacting a sample, tissue, cell, or organism with the compounds of the present invention, measuring the nucleic acid or protein level of HIF1α or HIF2α and/or a related phenotypic or chemical endpoint at some time after treatment, and optionally comparing the measured value to a non-treated sample or sample treated with a further compound of the invention. These methods can also be performed in parallel or in combination with other experiments to determine the function of unknown genes for the process of target validation or to determine the validity of a particular gene product as a target for treatment or prevention of a particular disease, condition, or phenotype.

**E. Kits, Research Reagents, Diagnostics, and Therapeutics**

**[0091]** The compounds of the present invention can be utilized for diagnostics, therapeutics, prophylaxis and as research reagents and kits. Furthermore, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used by those of ordinary skill to elucidate the function of particular genes or to distinguish between functions of various members of a biological pathway.

**[0092]** For use in kits and diagnostics, the compounds of the present invention, either alone or in combination with other compounds or therapeutics, can be used as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion or the entire complement of genes expressed within cells and tissues.

**[0093]** As one nonlimiting example, expression patterns within cells or tissues treated with one or more antisense compounds are compared to control cells or tissues not treated with antisense compounds and the patterns produced are analyzed for differential levels of gene expression as they pertain, for example, to disease association, signaling pathway, cellular localization, expression level, size, structure or function of the genes examined. These analyses can be performed on stimulated or unstimulated cells and in the presence or absence of other compounds which affect expression patterns.

**[0094]** Examples of methods of gene expression analysis known in the art include DNA arrays or microarrays (Brazma and Vilo, *FEBS Lett.*, **2000,** 480, 17-24; Celis, *et al.*, *FEBS Lett.*, **2000,** 480, 2-16), SAGE (serial analysis of gene expression)(Madden, *et al.*, *Drug Discov. Today,* **2000,** 5, 415-425), READS (restriction enzyme amplification of digested cDNAs) (Prashar and Weissman, *Methods Enzymol.*, **1999,** 303, 258-72), TOGA (total gene expression analysis) (Sutcliffe, *et al.*, *Proc. Natl. Acad. Sci. U. S. A.*, **2000,** 97, 1976-81), protein arrays and proteomics (Celis, *et al.*, *FEBS Lett.*, **2000,** 480, 2-16; Jungblut, *et al.*, *Electrophoresis,* **1999,** 20, 2100-10), expressed sequence tag (EST) sequencing (Celis, *et al.*, *FEBS Lett.*, **2000,** 480, 2-16; Larsson, *et al.*, *J. Biotechnol.*, **2000,** 80, 143-57), subtractive RNA fingerprinting (SuRF) (Fuchs, *et al.*, *Anal. Biochem.*, **2000,** 286, 91-98; Larson, *et al.*, *Cytometry,* **2000,** 41, 203-208),

subtractive cloning, differential display (DD) (Jurecic and Belmont, *Curr. Opin. Microbiol.*, **2000,** 3, 316-21), comparative genomic hybridization (Carulli, *et al.*, *J. Cell Biochem. Suppl.*, **1998,** 31, 286-96), FISH (fluorescent *in situ* hybridization) techniques (Going and Gusterson, *Eur. J. Cancer,* **1999,** 35, 1895-904) and mass spectrometry methods (To, *Comb. Chem. High Throughput Screen,* **2000,** 3, 235-41).

**[0095]** The compounds of the invention are useful for research and diagnostics, because these compounds hybridize to nucleic acids encoding HIF1α or HIF2α. For example, oligonucleotides that are shown to hybridize with such efficiency and under such conditions as disclosed herein as to be effective HIF1α or HIF2α inhibitors will also be effective primers or probes under conditions favoring gene amplification or detection, respectively. These primers and probes are useful in methods requiring the specific detection of nucleic acid molecules encoding HIF1α or HIF2α and in the amplification of said nucleic acid molecules for detection or for use in further studies of HIF1α or HIF2α. Hybridization of the antisense oligonucleotides, particularly the primers and probes, of the invention with a nucleic acid encoding HIF1α or HIF2α can be detected by means known in the art. Such means may include conjugation of an enzyme to the oligonucleotide, radiolabelling of the oligonucleotide or any other suitable detection means. Kits using such detection means for detecting the level of HIF1α or HIF2α in a sample may also be prepared.

**[0096]** The specificity and sensitivity of antisense is also harnessed by those of skill in the art for therapeutic uses. Antisense compounds have been employed as therapeutic moieties in the treatment of disease states in animals, including humans. Antisense oligonucleotide drugs, including ribozymes, have been safely and effectively

administered to humans and numerous clinical trials are presently underway. It is thus established that antisense compounds can be useful therapeutic modalities that can be configured to be useful in treatment regimes for the treatment of cells, tissues and animals, especially humans.

**[0097]** For therapeutics, an animal, preferably a human, suspected of having a disease or disorder which can be treated by modulating the expression of HIF1α or HIF2α is treated by administering one or more antisense compounds in accordance with this invention. For example, in one non-limiting embodiment, the methods comprise the step of administering to the animal in need of treatment, a therapeutically effective amount of a HIF1α or HIF2α inhibitor. The HIF1α or HIF2α inhibitors of the present invention effectively inhibit the activity of the HIF target protein or inhibit the expression of the HIF1α or HIF2α protein. In one embodiment, the activity or expression of HIF1α or HIF2α in an animal is inhibited by about 10%. Preferably, the activity or expression of HIF1α or HIF2α in an animal is inhibited by about 30%. More preferably, the activity or expression of HIF1α and/or HIF2α in an animal is inhibited by 50% or more.

**[0098]** For example, the reduction of the expression of HIF1α may be measured in serum, adipose tissue, liver or any other body fluid, tissue or organ of the animal. Preferably, the cells contained within said fluids, tissues or organs being analyzed contain a nucleic acid molecule encoding HIF1α or HIF2α protein and/or the HIF1α or HIF2α protein itself.

**[0099]** The compounds of the invention can be utilized in pharmaceutical compositions by adding an effective amount of a compound to a suitable pharmaceutically acceptable

diluent or carrier. Use of the compounds and methods of the invention may also be useful prophylactically.

**F. Modifications**

**[0100]** As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn, the respective ends of this linear polymeric compound can be further joined to form a circular compound, however, linear compounds are generally preferred. In addition, linear compounds may have internal nucleobase complementarity and may therefore fold in a manner as to produce a fully or partially double-stranded compound. Within oligonucleotides, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

*Modified Internucleoside Linkages (Backbones)*

**[0101]** Specific examples of preferred antisense compounds useful in this invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a

phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

**[0102]** Preferred modified oligonucleotide backbones containing a phosphorus atom therein include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, selenophosphates and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e. a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included.

**[0103]** Representative United States patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S.: 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697 and 5,625,050, certain of

which are commonly owned with this application, and each of which is herein incorporated by reference.

**[0104]** Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and $CH_2$ component parts.

**[0105]** Representative United States patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S.: 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269 and 5,677,439, certain of which are commonly owned with this application, and each of which is herein incorporated by reference.

*Modified sugar and internucleoside linkages-Mimetics*

**[0106]** In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage (i.e. the backbone), of the nucleotide units are replaced with novel

groups. The nucleobase units are maintained for hybridization with an appropriate target nucleic acid. One such compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S.: 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen *et al.*, *Science*, **1991**, 254, 1497-1500.

**[0107]** Preferred embodiments of the invention are oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular $-CH_2-NH-O-CH_2-$, $-CH_2-N(CH_3)-O-CH_2-$ [known as a methylene (methylimino) or MMI backbone], $-CH_2-O-N(CH_3)-CH_2-$, $-CH_2-N(CH_3)-N(CH_3)-CH_2-$ and $-O-N(CH_3)-CH_2-CH_2-$ [wherein the native phosphodiester backbone is represented as $-O-P-O-CH_2-$] of the above referenced U.S. patent 5,489,677, and the amide backbones of the above referenced U.S. patent 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced U.S. patent 5,034,506.

*Modified sugars*

**[0108]** Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-

, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted $C_1$ to $C_{10}$ alkyl or $C_2$ to $C_{10}$ alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3]_2$, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: $C_1$ to $C_{10}$ lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, $SCH_3$, OCN, Cl, Br, CN, $CF_3$, $OCF_3$, $SOCH_3$, $SO_2CH_3$, $ONO_2$, $NO_2$, $N_3$, $NH_2$, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O-$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*, **1995**, *78*, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethyl-amino-ethoxy-ethyl or 2'-DMAEOE), i.e., 2'-O-$CH_2$-O-$CH_2$-$N(CH_3)_2$, also described in examples hereinbelow.

**[0109]** Other preferred modifications include 2'-methoxy (2'-O-$CH_3$), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$), 2'-allyl (2'-$CH_2$-CH=$CH_2$), 2'-O-allyl (2'-O-$CH_2$-CH=$CH_2$) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal

nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 5,792,747; and 5,700,920, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

**[0110]** A further preferred modification of the sugar includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring, thereby forming a bicyclic sugar moiety. The linkage is preferably a methylene $(-CH_2-)_n$ group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226.

*Natural and Modified Nucleobases*

**[0111]** Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine

and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl (-C≡C-$CH_3$) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines such as phenoxazine cytidine(1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in United States Patent No. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, **1990**, those disclosed by Englisch *et al.*, *Angewandte Chemie*, International Edition, **1991**, *30*, 613, and those disclosed by Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, pages 289-302, Crooke, S.T. and Lebleu, B. , ed., CRC Press, **1993**. Certain of these nucleobases are particularly useful for increasing the binding affinity of the compounds of the invention. These include 5-substituted

pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2 °C and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

**[0112]** Representative United States patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. 3,687,808, as well as U.S.: 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; and 5,681,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference, and United States patent 5,750,692, which is commonly owned with the instant application and also herein incorporated by reference.

*Conjugates*

**[0113]** Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. These moieties or conjugates can include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the

pharmacokinetic properties of oligomers. Typical conjugate groups include cholesterols, lipids, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve uptake, enhance resistance to degradation, and/or strengthen sequence-specific hybridization with the target nucleic acid. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve uptake, distribution, metabolism or excretion of the compounds of the present invention. Representative conjugate groups are disclosed in International Patent Application PCT/US92/09196, filed October 23, 1992, and U.S. Patent 6,287,860, the entire disclosure of which are incorporated herein by reference. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g., hexyl-S-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (*S*)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in United

States Patent Application 09/334,130 (filed June 15, 1999) which is incorporated herein by reference in its entirety.

**[0114]** Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S.: 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

*Chimeric compounds*

**[0115]** It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide.

**[0116]** The present invention also includes antisense compounds which are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides

typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, increased stability and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNAse H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide-mediated inhibition of gene expression. The cleavage of RNA:RNA hybrids can, in like fashion, be accomplished through the actions of endoribonucleases, such as RNAseL which cleaves both cellular and viral RNA. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

**[0117]** Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids or gapmers. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S.: 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference in its entirety.

**G. Formulations**

The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor-targeted molecules, oral, rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption-assisting formulations include, but are not limited to, U.S.: 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

**[0118]** The antisense compounds of the invention encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to prodrugs and pharmaceutically acceptable salts of the compounds of the invention, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. The term "prodrug" indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions. In particular, prodrug versions of the oligonucleotides of the invention are prepared as SATE [(S-acetyl-2-thioethyl) phosphate] derivatives according to

the methods disclosed in WO 93/24510 to Gosselin *et al.*, published December 9, 1993 or in WO 94/26764 and U.S. 5,770,713 to Imbach *et al.*

**[0119]** The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto. For oligonucleotides, preferred examples of pharmaceutically acceptable salts and their uses are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety.

**[0120]** The present invention also includes pharmaceutical compositions and formulations which include the antisense compounds of the invention. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including vaginal and rectal delivery), pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration. Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration. Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily

bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful.

**[0121]** The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

**[0122]** The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

**[0123]** Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, foams and liposome-containing formulations. The pharmaceutical compositions and formulations of the present invention may comprise one or more penetration enhancers, carriers, excipients or other active or inactive ingredients.

**[0124]** Emulsions are typically heterogenous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter. Emulsions may contain additional components in addition to the dispersed phases,

and the active drug which may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Microemulsions are included as an embodiment of the present invention. Emulsions and their uses are well known in the art and are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety.

**[0125]** Formulations of the present invention include liposomal formulations. As used in the present invention, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers. Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior that contains the composition to be delivered. Cationic liposomes are positively charged liposomes which are believed to interact with negatively charged DNA molecules to form a stable complex. Liposomes that are pH-sensitive or negatively-charged are believed to entrap DNA rather than complex with it. Both cationic and noncationic liposomes have been used to deliver DNA to cells.

**[0126]** Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome comprises one or more glycolipids or is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. Liposomes and their uses are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety.

**[0127]** The pharmaceutical formulations and compositions of the present invention may also include

surfactants. The use of surfactants in drug products, formulations and in emulsions is well known in the art. Surfactants and their uses are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety.

**[0128]** In one embodiment, the present invention employs various penetration enhancers to effect the efficient delivery of nucleic acids, particularly oligonucleotides. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs. Penetration enhancers may be classified as belonging to one of five broad categories, *i.e.*, surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants. Penetration enhancers and their uses are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety.

**[0129]** One of skill in the art will recognize that formulations are routinely designed according to their intended use, i.e. route of administration.

**[0130]** Preferred formulations for topical administration include those in which the oligonucleotides of the invention are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Preferred lipids and liposomes include neutral (e.g. dioleoylphosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearolyphosphatidyl choline) negative (e.g. dimyristoylphosphatidyl glycerol DMPG) and cationic (e.g. dioleoyltetramethylaminopropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA).

**[0131]** For topical or other administration, oligonucleotides of the invention may be encapsulated within liposomes or may form complexes thereto, in particular to

cationic liposomes. Alternatively, oligonucleotides may be complexed to lipids, in particular to cationic lipids. Preferred fatty acids and esters, pharmaceutically acceptable salts thereof, and their uses are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety. Topical formulations are described in detail in United States patent application 09/315,298 filed on May 20, 1999, which is incorporated herein by reference in its entirety.

**[0132]** Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. Preferred oral formulations are those in which oligonucleotides of the invention are administered in conjunction with one or more penetration enhancers surfactants and chelators. Preferred surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Preferred bile acids/salts and fatty acids and their uses are further described in U.S. Patent 6,287,860, which is incorporated herein in its entirety. Also preferred are combinations of penetration enhancers, for example, fatty acids/salts in combination with bile acids/salts. A particularly preferred combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. Oligonucleotides of the invention may be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. Oligonucleotide complexing agents and their uses are further described in U.S. Patent 6,287,860, which is

incorporated herein in its entirety. Oral formulations for oligonucleotides and their preparation are described in detail in United States applications 09/108,673 (filed July 1, 1998), 09/315,298 (filed May 20, 1999) and 10/071,822, filed February 8, 2002, each of which is incorporated herein by reference in their entirety.

**[0133]** Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

**[0134]** Certain embodiments of the invention provide pharmaceutical compositions containing one or more oligomeric compounds and one or more other chemotherapeutic agents which function by a non-antisense mechanism. Examples of such chemotherapeutic agents include but are not limited to cancer chemotherapeutic drugs such as daunorubicin, daunomycin, dactinomycin, doxorubicin, epirubicin, idarubicin, esorubicin, bleomycin, mafosfamide, ifosfamide, cytosine arabinoside, bis-chloroethylnitrosurea, busulfan, mitomycin C, actinomycin D, mithramycin, prednisone, hydroxyprogesterone, testosterone, tamoxifen, dacarbazine, procarbazine, hexamethylmelamine, pentamethylmelamine, mitoxantrone, amsacrine, chlorambucil, methylcyclohexylnitrosurea, nitrogen mustards, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-azacytidine, hydroxyurea, deoxycoformycin, 4-hydroxyperoxycyclophosphoramide, 5-fluorouracil (5-FU), 5-fluorodeoxyuridine (5-FUdR), methotrexate (MTX), colchicine, taxol, vincristine, vinblastine, etoposide (VP-16), trimetrexate, irinotecan, topotecan, gemcitabine, teniposide, cisplatin and diethylstilbestrol (DES). When used with the compounds of the invention, such chemotherapeutic

agents may be used individually (*e.g.*, 5-FU and oligonucleotide), sequentially (*e.g.*, 5-FU and oligonucleotide for a period of time followed by MTX and oligonucleotide), or in combination with one or more other such chemotherapeutic agents (*e.g.*, 5-FU, MTX and oligonucleotide, or 5-FU, radiotherapy and oligonucleotide). Anti-inflammatory drugs, including but not limited to nonsteroidal anti-inflammatory drugs and corticosteroids, and antiviral drugs, including but not limited to ribivirin, vidarabine, acyclovir and ganciclovir, may also be combined in compositions of the invention. Combinations of antisense compounds and other non-antisense drugs are also within the scope of this invention. Two or more combined compounds may be used together or sequentially.

**[0135]** In another related embodiment, compositions of the invention may contain one or more antisense compounds, particularly oligonucleotides, targeted to a first nucleic acid and one or more additional antisense compounds targeted to a second nucleic acid target. Alternatively, compositions of the invention may contain two or more antisense compounds targeted to different regions of the same nucleic acid target. Numerous examples of antisense compounds are known in the art. Two or more combined compounds may be used together or sequentially.

**H. Dosing**

**[0136]** The formulation of therapeutic compositions and their subsequent administration (dosing) is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing

schedules can be calculated from measurements of drug accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on $EC_{50}$s found to be effective in *in vitro* and *in vivo* animal models. In general, dosage is from 0.01 ug to 100 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 ug to 100 g per kg of body weight, once or more daily, to once every 20 years.

**[0137]** While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following examples serve only to illustrate the invention and are not intended to limit the same.

**EXAMPLES**

**Example 1**

**Synthesis of Nucleoside Phosphoramidites**

**[0138]** The following compounds, including amidites and their intermediates were prepared as described in US Patent 6,426,220 and published PCT WO 02/36743; 5'-O-Dimethoxytrityl-thymidine intermediate for 5-methyl dC amidite, 5'-O-Dimethoxytrityl-2'-deoxy-5-methylcytidine intermediate for 5-methyl-dC amidite, 5'-O-Dimethoxytrityl-2'-deoxy-N4-benzoyl-5-methylcytidine penultimate intermediate for 5-methyl dC amidite, [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-deoxy-$N^4$-benzoyl-5-methylcytidin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (5-methyl dC amidite), 2'-Fluorodeoxyadenosine, 2'-Fluorodeoxyguanosine, 2'-Fluorouridine, 2'-Fluorodeoxycytidine, 2'-O-(2-Methoxyethyl) modified amidites, 2'-O-(2-methoxyethyl)-5-methyluridine intermediate, 5'-O-DMT-2'-O-(2-methoxyethyl)-5-methyluridine penultimate intermediate, [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-5-methyluridin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE T amidite), 5'-O-Dimethoxytrityl-2'-O-(2-methoxyethyl)-5-methylcytidine intermediate, 5'-O-dimethoxytrityl-2'-*O*-(2-methoxyethyl)-$N^4$-benzoyl-5-methyl-cytidine penultimate intermediate, [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-$N^4$-benzoyl-5-methylcytidin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE 5-Me-C amidite), [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-$N^6$-benzoyladenosin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE A amdite), [5'-*O*-(4,4'-Dimethoxytriphenylmethyl)-2'-*O*-(2-methoxyethyl)-$N^4$-

isobutyrylguanosin-3'-*O*-yl]-2-cyanoethyl-*N,N*-diisopropylphosphoramidite (MOE G amidite), 2'-O-(Aminooxyethyl) nucleoside amidites and 2'-O-(dimethylamino-oxyethyl) nucleoside amidites, 2'-(Dimethylaminooxyethoxy) nucleoside amidites, 5'-O-tert-Butyldiphenylsilyl-$O^2$-2'-anhydro-5-methyluridine , 5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine, 2'-O-([2-phthalimidoxy)ethyl]-5'-*t*-butyldiphenylsilyl-5-methyluridine , 5'-O-*tert*-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy)ethyl]-5-methyluridine, 5'-O-*tert*-Butyldiphenylsilyl-2'-O-[N,N dimethylaminooxyethyl]-5-methyluridine, 2'-O-(dimethylaminooxyethyl)-5-methyluridine, 5'-O-DMT-2'-O-(dimethylaminooxyethyl)-5-methyluridine, 5'-O-DMT-2'-O-(2-N,N-dimethylaminooxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite], 2'-(Aminooxyethoxy) nucleoside amidites, N2-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite], 2'-dimethylaminoethoxyethoxy (2'-DMAEOE) nucleoside amidites, 2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl]-5-methyl uridine, 5'-O-dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)-ethyl)]-5-methyl uridine and 5'-O-Dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)-ethyl)]-5-methyl uridine-3'-O-(cyanoethyl-N,N-diisopropyl)phosphoramidite.

**Example 2**

**Oligonucleotide and oligonucleoside synthesis**

**[0139]** The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA).

Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives.

**[0140]** Oligonucleotides: Unsubstituted and substituted phosphodiester (P=O) oligonucleotides are synthesized on an automated DNA synthesizer (Applied Biosystems model 394) using standard phosphoramidite chemistry with oxidation by iodine.

**[0141]** Phosphorothioates (P=S) are synthesized similar to phosphodiester oligonucleotides with the following exceptions: thiation was effected by utilizing a 10% w/v solution of 3,H-1,2-benzodithiole-3-one 1,1-dioxide in acetonitrile for the oxidation of the phosphite linkages. The thiation reaction step time was increased to 180 sec and preceded by the normal capping step. After cleavage from the CPG column and deblocking in concentrated ammonium hydroxide at 55°C (12-16 hr), the oligonucleotides were recovered by precipitating with >3 volumes of ethanol from a 1 M $NH_4OAc$ solution. Phosphinate oligonucleotides are prepared as described in U.S. Patent 5,508,270, herein incorporated by reference.

**[0142]** Alkyl phosphonate oligonucleotides are prepared as described in U.S. Patent 4,469,863, herein incorporated by reference.

**[0143]** 3'-Deoxy-3'-methylene phosphonate oligonucleotides are prepared as described in U.S. Patents 5,610,289 or 5,625,050, herein incorporated by reference.

**[0144]** Phosphoramidite oligonucleotides are prepared as described in U.S. Patent, 5,256,775 or U.S. Patent 5,366,878, herein incorporated by reference.

**[0145]** Alkylphosphonothioate oligonucleotides are prepared as described in published PCT applications PCT/US94/00902 and PCT/US93/06976 (published as WO 94/17093 and WO 94/02499, respectively), herein incorporated by reference.

**[0146]** 3'-Deoxy-3'-amino phosphoramidate oligonucleotides are prepared as described in U.S. Patent 5,476,925, herein incorporated by reference.

**[0147]** Phosphotriester oligonucleotides are prepared as described in U.S. Patent 5,023,243, herein incorporated by reference.

**[0148]** Borano phosphate oligonucleotides are prepared as described in U.S. Patents 5,130,302 and 5,177,198, both herein incorporated by reference.

**[0149]** Oligonucleosides: Methylenemethylimino linked oligonucleosides, also identified as MMI linked oligonucleosides, methylenedimethylhydrazo linked oligonucleosides, also identified as MDH linked oligonucleosides, and methylenecarbonylamino linked oligonucleosides, also identified as amide-3 linked oligonucleosides, and methyleneaminocarbonyl linked oligonucleosides, also identified as amide-4 linked oligonucleosides, as well as mixed backbone compounds having, for instance, alternating MMI and P=O or P=S linkages are prepared as described in U.S. Patents 5,378,825, 5,386,023, 5,489,677, 5,602,240 and 5,610,289, all of which are herein incorporated by reference.

**[0150]** Formacetal and thioformacetal linked oligonucleosides are prepared as described in U.S. Patents 5,264,562 and 5,264,564, herein incorporated by reference.

[0151] Ethylene oxide linked oligonucleosides are prepared as described in U.S. Patent 5,223,618, herein incorporated by reference.

**Example 3**

**RNA Synthesis**

[0152] In general, RNA synthesis chemistry is based on the selective incorporation of various protecting groups at strategic intermediary reactions. Although one of ordinary skill in the art will understand the use of protecting groups in organic synthesis, a useful class of protecting groups includes silyl ethers. In particular bulky silyl ethers are used to protect the 5′-hydroxyl in combination with an acid-labile orthoester protecting group on the 2′-hydroxyl. This set of protecting groups is then used with standard solid-phase synthesis technology. It is important to lastly remove the acid labile orthoester protecting group after all other synthetic steps. Moreover, the early use of the silyl protecting groups during synthesis ensures facile removal when desired, without undesired deprotection of 2′ hydroxyl.

[0153] Following this procedure for the sequential protection of the 5′-hydroxyl in combination with protection of the 2′-hydroxyl by protecting groups that are differentially removed and are differentially chemically labile, RNA oligonucleotides were synthesized.

[0154] RNA oligonucleotides are synthesized in a stepwise fashion. Each nucleotide is added sequentially (3′- to 5′-direction) to a solid support-bound oligonucleotide. The first nucleoside at the 3′-end of the chain is covalently attached to a solid support. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are added, coupling the second base onto the 5′-end of the first

nucleoside. The support is washed and any unreacted 5′-hydroxyl groups are capped with acetic anhydride to yield 5′-acetyl moieties. The linkage is then oxidized to the more stable and ultimately desired P(V) linkage. At the end of the nucleotide addition cycle, the 5′-silyl group is cleaved with fluoride. The cycle is repeated for each subsequent nucleotide.

**[0155]** Following synthesis, the methyl protecting groups on the phosphates are cleaved in 30 minutes utilizing 1 M disodium-2-carbamoyl-2-cyanoethylene-1,1-dithiolate trihydrate ($S_2Na_2$) in DMF. The deprotection solution is washed from the solid support-bound oligonucleotide using water. The support is then treated with 40% methylamine in water for 10 minutes at 55 °C. This releases the RNA oligonucleotides into solution, deprotects the exocyclic amines, and modifies the 2′- groups. The oligonucleotides can be analyzed by anion exchange HPLC at this stage.

**[0156]** The 2′-orthoester groups are the last protecting groups to be removed. The ethylene glycol monoacetate orthoester protecting group developed by Dharmacon Research, Inc. (Lafayette, CO), is one example of a useful orthoester protecting group which, has the following important properties. It is stable to the conditions of nucleoside phosphoramidite synthesis and oligonucleotide synthesis. However, after oligonucleotide synthesis the oligonucleotide is treated with methylamine which not only cleaves the oligonucleotide from the solid support but also removes the acetyl groups from the orthoesters. The resulting 2-ethyl-hydroxyl substituents on the orthoester are less electron withdrawing than the acetylated precursor. As a result, the modified orthoester becomes more labile to acid-catalyzed hydrolysis. Specifically, the rate of cleavage is approximately 10 times faster after the acetyl groups are

removed. Therefore, this orthoester possesses sufficient stability in order to be compatible with oligonucleotide synthesis and yet, when subsequently modified, permits deprotection to be carried out under relatively mild aqueous conditions compatible with the final RNA oligonucleotide product.

**[0157]** Additionally, methods of RNA synthesis are well known in the art (Scaringe, S. A. Ph.D. Thesis, University of Colorado, 1996; Scaringe, S. A., et al., *J. Am. Chem. Soc.*, **1998**, *120*, 11820-11821; Matteucci, M. D. and Caruthers, M. H. *J. Am. Chem. Soc.*, **1981**, *103*, 3185-3191; Beaucage, S. L. and Caruthers, M. H. *Tetrahedron Lett.*, **1981**, *22*, 1859-1862; Dahl, B. J., et al., *Acta Chem. Scand,.* **1990**, *44*, 639-641; Reddy, M. P., et al., *Tetrahedrom Lett.*, **1994**, *25*, 4311-4314; Wincott, F. et al., *Nucleic Acids Res.*, **1995**, *23*, 2677-2684; Griffin, B. E., et al., *Tetrahedron*, **1967**, *23*, 2301-2313; Griffin, B. E., et al., *Tetrahedron*, **1967**, *23*, 2315-2331).

**[0158]** RNA antisense compounds (RNA oligonucleotides) of the present invention can be synthesized by the methods herein or purchased from Dharmacon Research, Inc (Lafayette, CO). Once synthesized, complementary RNA antisense compounds can then be annealed by methods known in the art to form double stranded (duplexed) antisense compounds. For example, duplexes can be formed by combining 30 $\mu$l of each of the complementary strands of RNA oligonucleotides (50 uM RNA oligonucleotide solution) and 15 $\mu$l of 5X annealing buffer (100 mM potassium acetate, 30 mM HEPES-KOH pH 7.4, 2 mM magnesium acetate) followed by heating for 1 minute at 90°C, then 1 hour at 37°C. The resulting duplexed antisense compounds can be used in kits, assays, screens, or other methods to investigate the role of a target nucleic acid.

**Example 4**

**Synthesis of Chim ric Oligonucleotides**

**[0159]** Chimeric oligonucleotides, oligonucleosides or mixed oligonucleotides/oligonucleosides of the invention can be of several different types. These include a first type wherein the "gap" segment of linked nucleosides is positioned between 5′ and 3′ "wing" segments of linked nucleosides and a second "open end" type wherein the "gap" segment is located at either the 3′ or the 5′ terminus of the oligomeric compound. Oligonucleotides of the first type are also known in the art as "gapmers" or gapped oligonucleotides. Oligonucleotides of the second type are also known in the art as "hemimers" or "wingmers".

**[2′-O-Me]--[2′-deoxy]--[2′-O-Me] Chimeric Phosphorothioate Oligonucleotides**

**[0160]** Chimeric oligonucleotides having 2′-O-alkyl phosphorothioate and 2′-deoxy phosphorothioate oligonucleotide segments are synthesized using an Applied Biosystems automated DNA synthesizer Model 394, as above. Oligonucleotides are synthesized using the automated synthesizer and 2′-deoxy-5'-dimethoxytrityl-3'-O-phosphoramidite for the DNA portion and 5'-dimethoxytrityl-2'-O-methyl-3'-O-phosphoramidite for 5' and 3' wings. The standard synthesis cycle is modified by incorporating coupling steps with increased reaction times for the 5'-dimethoxytrityl-2'-O-methyl-3'-O-phosphoramidite. The fully protected oligonucleotide is cleaved from the support and deprotected in concentrated ammonia ($NH_4OH$) for 12-16 hr at 55ºC. The deprotected oligo is then recovered by an appropriate method (precipitation, column chromatography, volume reduced *in vacuo* and analyzed spetrophotometrically for yield and for purity by capillary electrophoresis and by mass spectrometry.

**[2'-O-(2-Methoxyethyl)]--[2'-deoxy]--[2'-O-(Methoxyethyl)] Chimeric Phosphorothioate Oligonucleotides**

**[0161]** [2'-O-(2-methoxyethyl)]--[2'-deoxy]--[-2'-O-(methoxyethyl)] chimeric phosphorothioate oligonucleotides were prepared as per the procedure above for the 2'-O-methyl chimeric oligonucleotide, with the substitution of 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites.

**[2'-O-(2-Methoxyethyl)Phosphodiester]--[2'-deoxy Phosphorothioate]--[2'-O-(2-Methoxyethyl) Phosphodiester] Chimeric Oligonucleotides**

**[0162]** [2'-O-(2-methoxyethyl phosphodiester]--[2'-deoxy phosphorothioate]--[2'-O-(methoxyethyl) phosphodiester] chimeric oligonucleotides are prepared as per the above procedure for the 2'-O-methyl chimeric oligonucleotide with the substitution of 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites, oxidation with iodine to generate the phosphodiester internucleotide linkages within the wing portions of the chimeric structures and sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) to generate the phosphorothioate internucleotide linkages for the center gap.

**[0163]** Other chimeric oligonucleotides, chimeric oligonucleosides and mixed chimeric oligonucleotides/oligonucleosides are synthesized according to United States patent 5,623,065, herein incorporated by reference.

**Example 5**

**Design and screening of duplexed antisense compounds targeting HIF1α or HIF2α**

**[0164]** In accordance with the present invention, a series of nucleic acid duplexes comprising the antisense compounds of the present invention and their complements can be designed to target HIF1α or HIF2α. The nucleobase sequence of the antisense strand of the duplex preferably comprises at least a portion of an oligonucleotide in Tables 1, 3, 4, 5, 6, 13, or 14. The ends of the strands may be modified by the addition of one or more natural or modified nucleobases to form an overhang. The sense strand of the dsRNA is then designed and synthesized as the complement of the antisense strand and may also contain modifications or additions to either terminus. For example, in one embodiment, both strands of the dsRNA duplex would be complementary over the central nucleobases, each having overhangs at one or both termini.

**[0165]** For example, a duplex comprising an antisense strand having the sequence CGAGAGGCGGACGGGACCG and having a two-nucleobase overhang of deoxythymidine(dT) would have the following structure:

```
cgagaggcggacgggaccgTT    Antisense Strand
||||||||||||||||||||
TTgctctccgcctgccctggc    Complement
```

**[0166]** As another example, a duplex comprising an antisense strand having the sequence CGAGAGGCGGACGGGACCG and having no overhangs would have the following structure:

```
cgagaggcggacgggaccg      Antisense Strand
|||||||||||||||||||
gctctccgcctgccctggc      Complement
```

**[0167]** RNA strands of the duplex can be synthesized by methods disclosed herein or purchased from Dharmacon Research Inc., (Lafayette, CO). Once synthesized, the complementary strands are annealed. The single strands are aliquoted and diluted to a concentration of 50 uM. Once diluted, 30 uL of each strand is combined with 15uL of a 5X solution of annealing buffer. The final concentration of said buffer is 100 mM potassium acetate, 30 mM HEPES-KOH pH 7.4, and 2mM magnesium acetate. The final volume is 75 uL. This solution is incubated for 1 minute at 90°C and then centrifuged for 15 seconds. The tube is allowed to sit for 1 hour at 37°C at which time the dsRNA duplexes are used in experimentation. The final concentration of the dsRNA duplex is 20 uM. This solution can be stored frozen (-20°C) and freeze-thawed up to 5 times.

**[0168]** Once prepared, the duplexed antisense compounds are evaluated for their ability to modulate HIF1• or HIF2• expression.

**[0169]** When cells reached 80% confluency, they are treated with duplexed antisense compounds of the invention. For cells grown in 96-well plates, wells are washed once with 200 •L OPTI-MEM-1 reduced-serum medium (Gibco BRL) and then treated with 130 •L of OPTI-MEM-1 containing 12 •g/mL LIPOFECTIN (Gibco BRL) and the desired duplex antisense compound at a final concentration of 200 nM. After 5 hours of treatment, the medium is replaced with fresh medium. Cells are harvested 16 hours after treatment, at which time RNA is isolated and target reduction measured by RT-PCR.

**Example 6**

**Oligonucleotide Isolation**

**[0170]** After cleavage from the controlled pore glass solid support and deblocking in concentrated ammonium hydroxide at 55°C for 12-16 hours, the oligonucleotides or

oligonucleosides are recovered by precipitation out of 1 M $NH_4OAc$ with >3 volumes of ethanol. Synthesized oligonucleotides were analyzed by electrospray mass spectroscopy (molecular weight determination) and by capillary gel electrophoresis and judged to be at least 70% full length material. The relative amounts of phosphorothioate and phosphodiester linkages obtained in the synthesis was determined by the ratio of correct molecular weight relative to the -16 amu product (+/-32 +/-48). For some studies oligonucleotides were purified by HPLC, as described by Chiang *et al.*, *J. Biol. Chem.* **1991**, *266*, 18162-18171. Results obtained with HPLC-purified material were similar to those obtained with non-HPLC purified material.

**Example 7**

**Oligonucleotide Synthesis - 96 Well Plate Format**

**[0171]** Oligonucleotides were synthesized via solid phase P(III) phosphoramidite chemistry on an automated synthesizer capable of assembling 96 sequences simultaneously in a 96-well format. Phosphodiester internucleotide linkages were afforded by oxidation with aqueous iodine. Phosphorothioate internucleotide linkages were generated by sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) in anhydrous acetonitrile. Standard base-protected beta-cyanoethyl-diiso-propyl phosphoramidites were purchased from commercial vendors (e.g. PE-Applied Biosystems, Foster City, CA, or Pharmacia, Piscataway, NJ). Non-standard nucleosides are synthesized as per standard or patented methods. They are utilized as base protected beta-cyanoethyldiisopropyl phosphoramidites.

**[0172]** Oligonucleotides were cleaved from support and deprotected with concentrated $NH_4OH$ at elevated temperature (55-60°C) for 12-16 hours and the released product then dried

*in vacuo*. The dried product was then re-suspended in sterile water to afford a master plate from which all analytical and test plate samples are then diluted utilizing robotic pipettors.

**Example 8**

**Oligonucleotide Analysis - 96-Well Plate Format**

**[0173]** The concentration of oligonucleotide in each well was assessed by dilution of samples and UV absorption spectroscopy. The full-length integrity of the individual products was evaluated by capillary electrophoresis (CE) in either the 96-well format (Beckman P/ACE™ MDQ) or, for individually prepared samples, on a commercial CE apparatus (e.g., Beckman P/ACE™ 5000, ABI 270). Base and backbone composition was confirmed by mass analysis of the compounds utilizing electrospray-mass spectroscopy. All assay test plates were diluted from the master plate using single and multi-channel robotic pipettors. Plates were judged to be acceptable if at least 85% of the compounds on the plate were at least 85% full length.

**Example 9**

**Cell culture and oligonucleotide treatment**

**[0174]** The effect of antisense compounds on target nucleic acid expression can be tested in any of a variety of cell types provided that the target nucleic acid is present at measurable levels. This can be routinely determined using, for example, PCR or Northern blot analysis. The following cell types are provided for illustrative purposes, but other cell types can be routinely used, provided that the target is expressed in the cell type chosen. This can be readily determined by methods routine in the art, for example

Northern blot analysis, ribonuclease protection assays, or RT-PCR.

T-24 cells:

**[0175]** The human transitional cell bladder carcinoma cell line T-24 was obtained from the American Type Culture Collection (ATCC) (Manassas, VA). T-24 cells were routinely cultured in complete McCoy's 5A basal media (Invitrogen Corporation, Carlsbad, CA) supplemented with 10% fetal calf serum (Invitrogen Corporation, Carlsbad, CA), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Invitrogen Corporation, Carlsbad, CA). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #353872) at a density of 7000 cells/well for use in RT-PCR analysis.

**[0176]** For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

A549 cells:

**[0177]** The human lung carcinoma cell line A549 was obtained from the American Type Culture Collection (ATCC) (Manassas, VA). A549 cells were routinely cultured in DMEM basal media (Invitrogen Corporation, Carlsbad, CA) supplemented with 10% fetal calf serum (Invitrogen Corporation, Carlsbad, CA), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Invitrogen Corporation, Carlsbad, CA). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence.

NHDF cells:

**[0178]** Human neonatal dermal fibroblast (NHDF) were obtained from the Clonetics Corporation (Walkersville, MD). NHDFs were routinely maintained in Fibroblast Growth Medium (Clonetics Corporation, Walkersville, MD) supplemented as recommended by the supplier. Cells were maintained for up to 10 passages as recommended by the supplier.

HEK cells:

**[0179]** Human embryonic keratinocytes (HEK) were obtained from the Clonetics Corporation (Walkersville, MD). HEKs were routinely maintained in Keratinocyte Growth Medium (Clonetics Corporation, Walkersville, MD) formulated as recommended by the supplier. Cells were routinely maintained for up to 10 passages as recommended by the supplier.

b.END cells:

**[0180]** The mouse brain endothelial cell line b.END was obtained from Dr. Werner Risau at the Max Plank Instititute (Bad Nauheim, Germany). b.END cells were routinely cultured in DMEM, high glucose (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD). Cells were routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells were seeded into 96-well plates (Falcon-Primaria #3872) at a density of 3000 cells/well for use in RT-PCR analysis.

**[0181]** For Northern blotting or other analyses, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

Treatment with antisense compounds:

**[0182]** When cells reached 65-75% confluency, they were treated with oligonucleotide. For cells grown in 96-well plates, wells were washed once with 100 µL OPTI-MEM™-1 reduced-serum medium (Invitrogen Corporation, Carlsbad, CA) and then treated with 130 µL of OPTI-MEM™-1 containing 3.75 µg/mL LIPOFECTIN™ (Invitrogen Corporation, Carlsbad, CA) and the desired concentration of oligonucleotide. Cells are treated and data are obtained in triplicate. After 4-7 hours of treatment at 37°C, the medium was replaced with fresh medium. Cells were harvested 16-24 hours after oligonucleotide treatment.

**[0183]** The concentration of oligonucleotide used varies from cell line to cell line. To determine the optimal oligonucleotide concentration for a particular cell line, the cells are treated with a positive control oligonucleotide at a range of concentrations. For human cells the positive control oligonucleotide is selected from either ISIS 13920 (**TCC**GTCATCGCT**CCTCAGGG**, SEQ ID NO: 1) which is targeted to human H-ras, or ISIS 18078, (**GTGCG**CGCGAGCCCG**AAATC**, SEQ ID NO: 2) which is targeted to human Jun-N-terminal kinase-2 (JNK2). Both controls are 2'-O-methoxyethyl gapmers (2'-O-methoxyethyls shown in bold) with a phosphorothioate backbone. For mouse or rat cells the positive control oligonucleotide is ISIS 15770, **ATGCA**TTCTGCCCCC**AAGGA**, SEQ ID NO: 3, a 2'-O-methoxyethyl gapmer (2'-O-methoxyethyls shown in bold) with a phosphorothioate backbone which is targeted to both mouse and rat c-raf. The concentration of positive control oligonucleotide that results in 80% inhibition of c-H-ras (for ISIS 13920), JNK2 (for ISIS 18078) or c-raf (for ISIS 15770) mRNA is then utilized as the screening concentration for new oligonucleotides in subsequent

experiments for that cell line. If 80% inhibition is not achieved, the lowest concentration of positive control oligonucleotide that results in 60% inhibition of c-H-ras, JNK2 or c-raf mRNA is then utilized as the oligonucleotide screening concentration in subsequent experiments for that cell line. If 60% inhibition is not achieved, that particular cell line is deemed as unsuitable for oligonucleotide transfection experiments. The concentrations of antisense oligonucleotides used herein are from 50 nM to 300 nM.

**Example 10**

**Analysis of oligonucleotide inhibition of HIF1α and/or HIF2α expression**

**[0184]** Antisense modulation of HIF1α and/or HIF2α expression can be assayed in a variety of ways known in the art. For example, HIF1α or HIF2α mRNA levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or real-time PCR (RT-PCR). Real-time quantitative PCR is presently preferred. RNA analysis can be performed on total cellular RNA or poly(A)+ mRNA. The preferred method of RNA analysis of the present invention is the use of total cellular RNA as described in other examples herein. Methods of RNA isolation are well known in the art. Northern blot analysis is also routine in the art. Real-time quantitative (PCR) can be conveniently accomplished using the commercially available ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions.

**[0185]** Protein levels of HIF1α or HIF2α can be quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis

(immunoblotting), enzyme-linked immunosorbent assay (ELISA) or fluorescence-activated cell sorting (FACS). Antibodies directed to HIF1α or HIF2α can be identified and obtained from a variety of sources, such as the MSRS catalog of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional monoclonal or polyclonal antibody generation methods well known in the art.

**Example 11**

**Design of phenotypic assays and *in vivo* studies for the use of HIF1α or HIF2α inhibitors**

*Phenotypic assays*

**[0186]** Once HIF1α or HIF2α inhibitors have been identified by the methods disclosed herein, the compounds are further investigated in one or more phenotypic assays, each having measurable endpoints predictive of efficacy in the treatment of a particular disease state or condition.

**[0187]** Phenotypic assays, kits and reagents for their use are well known to those skilled in the art and are herein used to investigate the role and/or association of HIF1α and/or HIF2α in health and disease. Representative phenotypic assays, which can be purchased from any one of several commercial vendors, include those for determining cell viability, cytotoxicity, proliferation or cell survival (Molecular Probes, Eugene, OR; PerkinElmer, Boston, MA), protein-based assays including enzymatic assays (Panvera, LLC, Madison, WI; BD Biosciences, Franklin Lakes, NJ; Oncogene Research Products, San Diego, CA), cell regulation, signal transduction, inflammation, oxidative processes and apoptosis (Assay Designs Inc., Ann Arbor, MI), triglyceride accumulation (Sigma-Aldrich, St. Louis, MO), angiogenesis assays, tube formation assays, cytokine and hormone assays

and metabolic assays (Chemicon International Inc., Temecula, CA; Amersham Biosciences, Piscataway, NJ).

**[0188]** In one non-limiting example, cells determined to be appropriate for a particular phenotypic assay (i.e., MCF-7 cells selected for breast cancer studies; adipocytes for obesity studies) are treated with HIF1α and/or HIF2α inhibitors identified from the *in vitro* studies as well as control compounds at optimal concentrations which are determined by the methods described above. At the end of the treatment period, treated and untreated cells are analyzed by one or more methods specific for the assay to determine phenotypic outcomes and endpoints.

**[0189]** Phenotypic endpoints include changes in cell morphology over time or treatment dose as well as changes in levels of cellular components such as proteins, lipids, nucleic acids, hormones, saccharides or metals. Measurements of cellular status which include pH, stage of the cell cycle, intake or excretion of biological indicators by the cell, are also endpoints of interest.

**[0190]** Analysis of the geneotype of the cell (measurement of the expression of one or more of the genes of the cell) after treatment is also used as an indicator of the efficacy or potency of the HIF1α and/or HIF2α inhibitors. Hallmark genes, or those genes suspected to be associated with a specific disease state, condition, or phenotype, are measured in both treated and untreated cells.

**Example 12**

**RNA Isolation**

*Poly(A)+ mRNA isolation*

**[0191]** Poly(A)+ mRNA was isolated according to Miura *et al.*, (*Clin. Chem.*, **1996**, *42*, 1758-1764). Other methods

for poly(A)+ mRNA isolation are routine in the art. Briefly, for cells grown on 96-well plates, growth medium was removed from the cells and each well was washed with 200 µL cold PBS. 60 µL lysis buffer (10 mM Tris-HCl, pH 7.6, 1 mM EDTA, 0.5 M NaCl, 0.5% NP-40, 20 mM vanadyl-ribonucleoside complex) was added to each well, the plate was gently agitated and then incubated at room temperature for five minutes. 55 µL of lysate was transferred to Oligo d(T) coated 96-well plates (AGCT Inc., Irvine CA). Plates were incubated for 60 minutes at room temperature, washed 3 times with 200 µL of wash buffer (10 mM Tris-HCl pH 7.6, 1 mM EDTA, 0.3 M NaCl). After the final wash, the plate was blotted on paper towels to remove excess wash buffer and then air-dried for 5 minutes. 60 µL of elution buffer (5 mM Tris-HCl pH 7.6), preheated to 70°C, was added to each well, the plate was incubated on a 90°C hot plate for 5 minutes, and the eluate was then transferred to a fresh 96-well plate.

**[0192]** Cells grown on 100 mm or other standard plates may be treated similarly, using appropriate volumes of all solutions.

*Total RNA Isolation*

**[0193]** Total RNA was isolated using an RNEASY 96™ kit and buffers purchased from Qiagen Inc. (Valencia, CA) following the manufacturer's recommended procedures. Briefly, for cells grown on 96-well plates, growth medium was removed from the cells and each well was washed with 200 µL cold PBS. 150 µL Buffer RLT was added to each well and the plate vigorously agitated for 20 seconds. 150 µL of 70% ethanol was then added to each well and the contents mixed by pipetting three times up and down. The samples were then transferred to the RNEASY 96™ well plate attached to a

QIAVAC™ manifold fitted with a waste collection tray and attached to a vacuum source. Vacuum was applied for 1 minute. 500 µL of Buffer RW1 was added to each well of the RNEASY 96™ plate and incubated for 15 minutes and the vacuum was again applied for 1 minute. An additional 500 µL of Buffer RW1 was added to each well of the RNEASY 96™ plate and the vacuum was applied for 2 minutes. 1 mL of Buffer RPE was then added to each well of the RNEASY 96™ plate and the vacuum applied for a period of 90 seconds. The Buffer RPE wash was then repeated and the vacuum was applied for an additional 3 minutes. The plate was then removed from the QIAVAC™ manifold and blotted dry on paper towels. The plate was then re-attached to the QIAVAC™ manifold fitted with a collection tube rack containing 1.2 mL collection tubes. RNA was then eluted by pipetting 140 µL of RNAse free water into each well, incubating 1 minute, and then applying the vacuum for 3 minutes.

**[0194]** The repetitive pipetting and elution steps may be automated using a QIAGEN Bio-Robot 9604 (Qiagen, Inc., Valencia CA). Essentially, after lysing of the cells on the culture plate, the plate is transferred to the robot deck where the pipetting, DNase treatment and elution steps are carried out.

**Example 13**

**Real-time Quantitative PCR Analysis of HIF1α mRNA Levels**

**[0195]** Quantitation of HIF1α mRNA levels was accomplished by real-time quantitative PCR using the ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. This is a closed-tube, non-gel-based, fluorescence detection system which allows high-

throughput quantitation of polymerase chain reaction (PCR) products in real-time. As opposed to standard PCR in which amplification products are quantitated after the PCR is completed, products in real-time quantitative PCR are quantitated as they accumulate. This is accomplished by including in the PCR reaction an oligonucleotide probe that anneals specifically between the forward and reverse PCR primers, and contains two fluorescent dyes. A reporter dye (e.g., FAM or JOE, obtained from either PE-Applied Biosystems, Foster City, CA, Operon Technologies Inc., Alameda, CA or Integrated DNA Technologies Inc., Coralville, IA) is attached to the 5' end of the probe and a quencher dye (e.g., TAMRA, obtained from either PE-Applied Biosystems, Foster City, CA, Operon Technologies Inc., Alameda, CA or Integrated DNA Technologies Inc., Coralville, IA) is attached to the 3' end of the probe. When the probe and dyes are intact, reporter dye emission is quenched by the proximity of the 3' quencher dye. During amplification, annealing of the probe to the target sequence creates a substrate that can be cleaved by the 5'-exonuclease activity of Taq polymerase. During the extension phase of the PCR amplification cycle, cleavage of the probe by Taq polymerase releases the reporter dye from the remainder of the probe (and hence from the quencher moiety) and a sequence-specific fluorescent signal is generated. With each cycle, additional reporter dye molecules are cleaved from their respective probes, and the fluorescence intensity is monitored at regular intervals by laser optics built into the ABI PRISM™ Sequence Detection System. In each assay, a series of parallel reactions containing serial dilutions of mRNA from untreated control samples generates a standard curve that is used to quantitate the percent inhibition after antisense oligonucleotide treatment of test samples.

**[0196]** Prior to quantitative PCR analysis, primer-probe sets specific to the target gene being measured are evaluated for their ability to be "multiplexed" with a GAPDH amplification reaction. In multiplexing, both the target gene and the internal standard gene GAPDH are amplified concurrently in a single sample. In this analysis, mRNA isolated from untreated cells is serially diluted. Each dilution is amplified in the presence of primer-probe sets specific for GAPDH only, target gene only ("single-plexing"), or both (multiplexing). Following PCR amplification, standard curves of GAPDH and target mRNA signal as a function of dilution are generated from both the single-plexed and multiplexed samples. If both the slope and correlation coefficient of the GAPDH and target signals generated from the multiplexed samples fall within 10% of their corresponding values generated from the single-plexed samples, the primer-probe set specific for that target is deemed multiplexable. Other methods of PCR are also known in the art.

**[0197]** PCR reagents were obtained from Invitrogen Corporation, (Carlsbad, CA). RT-PCR reactions were carried out by adding 20 μL PCR cocktail (2.5x PCR buffer minus $MgCl_2$, 6.6 mM $MgCl_2$, 375 μM each of dATP, dCTP, dCTP and dGTP, 375 nM each of forward primer and reverse primer, 125 nM of probe, 4 Units RNAse inhibitor, 1.25 Units PLATINUM® Taq, 5 Units MuLV reverse transcriptase, and 2.5x ROX dye) to 96-well plates containing 30 μL total RNA solution (20-200 ng). The RT reaction was carried out by incubation for 30 minutes at 48°C. Following a 10 minute incubation at 95°C to activate the PLATINUM® Taq, 40 cycles of a two-step PCR protocol were carried out: 95°C for 15 seconds (denaturation) followed by 60°C for 1.5 minutes (annealing/extension).

**[0198]** Gene target quantities obtained by real time RT-PCR are normalized using either the expression level of GAPDH, a gene whose expression is constant, or by quantifying total RNA using RiboGreen™ (Molecular Probes, Inc. Eugene, OR). GAPDH expression is quantified by real time RT-PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA is quantified using RiboGreen™ RNA quantification reagent (Molecular Probes, Inc. Eugene, OR). Methods of RNA quantification by RiboGreen™ are taught in Jones, L.J., et al, (Analytical Biochemistry, 1998, 265, 368-374).

**[0199]** In this assay, 170 μL of RiboGreen™ working reagent (RiboGreen™ reagent diluted 1:350 in 10mM Tris-HCl, 1 mM EDTA, pH 7.5) is pipetted into a 96-well plate containing 30 μL purified, cellular RNA. The plate is read in a CytoFluor 4000 (PE Applied Biosystems) with excitation at 485nm and emission at 530nm.

**[0200]** Probes and primers to human HIF1α were designed to hybridize to a human HIF1α sequence, using published sequence information (GenBank accession number U29165.1, incorporated herein by reference and incorporated herein as SEQ ID NO:4). For human HIF1α the PCR primers were:
forward primer: CCAGTTACGTTCCTTCGATCAGT (SEQ ID NO: 5)
reverse primer: TTTGAGGACTTGCGCTTTCA (SEQ ID NO: 6) and the PCR probe was: FAM-TCACCATTAGAAAGCAGTTCCGCAAGCC-TAMRA (SEQ ID NO: 7) where FAM is the fluorescent dye and TAMRA is the quencher dye. For human GAPDH the PCR primers were:
forward primer: GAAGGTGAAGGTCGGAGTC(SEQ ID NO:8)
reverse primer: GAAGATGGTGATGGGATTTC (SEQ ID NO:9) and the PCR probe was: 5′ JOE-CAAGCTTCCCGTTCTCAGCC- TAMRA 3′ (SEQ ID NO: 10) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

**Example 14**

**Northern blot analysis of HIF1α mRNA levels**

**[0201]** Eighteen hours after antisense treatment, cell monolayers were washed twice with cold PBS and lysed in 1 mL RNAZOL™ (TEL-TEST "B" Inc., Friendswood, TX). Total RNA was prepared following manufacturer's recommended protocols. Twenty micrograms of total RNA was fractionated by electrophoresis through 1.2% agarose gels containing 1.1% formaldehyde using a MOPS buffer system (AMRESCO, Inc. Solon, OH). RNA was transferred from the gel to HYBOND™-N+ nylon membranes (Amersham Pharmacia Biotech, Piscataway, NJ) by overnight capillary transfer using a Northern/Southern Transfer buffer system (TEL-TEST "B" Inc., Friendswood, TX). RNA transfer was confirmed by UV visualization. Membranes were fixed by UV cross-linking using a STRATALINKER™ UV Crosslinker 2400 (Stratagene, Inc, La Jolla, CA) and then probed using QUICKHYB™ hybridization solution (Stratagene, La Jolla, CA) using manufacturer's recommendations for stringent conditions.

**[0202]** To detect human HIF1α, a human HIF1α specific probe was prepared by PCR using the forward primer CCAGTTACGTTCCTTCGATCAGT (SEQ ID NO: 5) and the reverse primer TTTGAGGACTTGCGCTTTCA (SEQ ID NO: 6). To normalize for variations in loading and transfer efficiency membranes were stripped and probed for human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

**[0203]** Hybridized membranes were visualized and quantitated using a PHOSPHORIMAGER™ and IMAGEQUANT™ Software V3.3 (Molecular Dynamics, Sunnyvale, CA). Data was normalized to GAPDH levels in untreated controls.

**Example 15**

**Antisense inhibition of human HIF1α expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

**[0204]** In accordance with the present invention, a series of antisense compounds were designed to target different regions of the human HIF1α RNA, using published sequences (GenBank accession number U29165.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 4, positions 82000 to 139500 of the sequence with GenBank accession number AL137129.4, incorporated herein by reference and incorporated herein as SEQ ID NO: 11, GenBank accession number AU123241.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 12, and GenBank accession number AB073325.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 13). The compounds are shown in Table 1. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 1 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on human HIF1α mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from three experiments in which A549 cells were treated with the antisense oligonucleotides of the present invention. If present, "N.D." indicates "no data".

**Table 1**

**Inhibition of human HIF1α mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

| ISIS # | REGION | TARGET SEQ ID NO | TARGET SITE | SEQUENCE | % INHIB | SEQ ID NO |
|---|---|---|---|---|---|---|
| 175477 | Coding | 4 | 2496 | aaagtgatgtagtagctgca | 54 | 14 |
| 175478 | Coding | 4 | 854 | ggtatcatatacgtgaatgt | 73 | 15 |
| 175479 | 3'UTR | 4 | 3179 | taccacgtactgctggcaaa | 31 | 16 |
| 175480 | Coding | 4 | 2039 | tgtgctttgaggacttgcgc | 94 | 17 |
| 175481 | Coding | 4 | 583 | gaaatgtaaatcatgtcacc | 56 | 18 |
| 175482 | Coding | 4 | 1408 | tcaaagaggctacttgtatc | 75 | 19 |
| 175483 | Coding | 4 | 1674 | ttaatgcaacttcttgattg | 45 | 20 |
| 175484 | 3'UTR | 4 | 3333 | atcattattatatgattaac | 60 | 21 |
| 175485 | 5'UTR | 4 | 152 | gaaaggcaagtccagaggtg | 42 | 22 |
| 175486 | 3'UTR | 4 | 3027 | taaactccctagccaaaaat | 40 | 23 |
| 175487 | Coding | 4 | 2085 | cattagcagtaggttcttgt | 75 | 24 |
| 175488 | 3'UTR | 4 | 3101 | gatcatgatgaaaggttact | 86 | 25 |
| 175489 | Coding | 4 | 1001 | aaatttcatatccaggctgt | 85 | 26 |
| 175490 | Coding | 4 | 460 | agtttcctcacacgcaaata | 38 | 27 |
| 175491 | Coding | 4 | 1983 | actgatcgaaggaacgtaac | 87 | 28 |
| 175492 | Coding | 4 | 2404 | cgctttctctgagcattctg | 44 | 29 |
| 175493 | Coding | 4 | 649 | aaatcaaacacactgtgtcc | 79 | 30 |
| 175494 | Coding | 4 | 1139 | tcctttagtaaacatatcat | 71 | 31 |
| 175495 | Coding | 4 | 1442 | caaagttaaagcatcaggtt | 79 | 32 |
| 175496 | Coding | 4 | 1765 | ctagtgcttccatcggaagg | 37 | 33 |
| 175497 | 3'UTR | 4 | 3424 | aatgccacataccttctaga | 24 | 34 |
| 175498 | 5'UTR | 4 | 110 | tcgtgagactagagagaagc | 71 | 35 |
| 175499 | 3'UTR | 4 | 3094 | atgaaaggttactgccttct | 81 | 36 |
| 175500 | Coding | 4 | 912 | tcagcaccaagcaggtcata | 8 | 37 |
| 175501 | 3'UTR | 4 | 2841 | aagtttgtgcagtattgtag | 33 | 38 |
| 175502 | Coding | 4 | 2396 | ctgagcattctgcaaagcta | 0 | 39 |
| 175503 | Coding | 4 | 350 | ttcagattctttacttcgcc | 54 | 40 |
| 175504 | Coding | 4 | 2320 | gataacacgttagggcttct | 41 | 41 |
| 175505 | Coding | 4 | 2331 | tcaaagcgacagataacacg | 51 | 42 |
| 175506 | Coding | 4 | 1091 | caaagcatgataatattcat | 56 | 43 |
| 175507 | Coding | 4 | 565 | ccatcatctgtgagaaccat | 86 | 44 |
| 175508 | Coding | 4 | 2222 | atatggtgatgatgtggcac | 76 | 45 |
| 175509 | 5'UTR | 4 | 51 | ctcctcaggtggcttgtcag | 33 | 46 |
| 175510 | 3'UTR | 4 | 2931 | tgagctgtctgtgatccagc | 94 | 47 |
| 175511 | Coding | 4 | 2321 | agataacacgttagggcttc | 86 | 48 |
| 175512 | Start Codon | 4 | 248 | catggtgaatcggtccccgc | 76 | 49 |
| 175513 | Coding | 4 | 1224 | tgttatatatgacagttgct | 73 | 50 |
| 224184 | Coding | 4 | 414 | ccttatcaagatgcgaactc | 63 | 51 |
| 224185 | Coding | 4 | 480 | ccaaatcaccagcatccaga | 32 | 52 |
| 224186 | Coding | 4 | 619 | aactgagttaatcccatgta | 72 | 53 |
| 224187 | Coding | 4 | 627 | ttagttcaaactgagttaat | 31 | 54 |
| 224188 | Coding | 4 | 706 | aggccatttctgtgtgtaag | 62 | 55 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 224189 | Coding | 4 | 961 | ctatctaaaggaatttcaat | 10 | 56 |
| 224190 | Coding | 4 | 1036 | cccatcaattcggtaattct | 41 | 57 |
| 224191 | Coding | 4 | 1125 | tatcatgatgagttttggtc | 81 | 58 |
| 224192 | Coding | 4 | 1283 | aataataccactcacaacgt | 60 | 59 |
| 224193 | Coding | 4 | 1380 | caactttggtgaatagctga | 71 | 60 |
| 224194 | Coding | 4 | 1699 | agtgactctggatttggttc | 44 | 61 |
| 224195 | Coding | 4 | 1928 | catctccaagtctaaatctg | 36 | 62 |
| 224196 | Coding | 4 | 1995 | ctaatggtgacaactgatcg | 72 | 63 |
| 224197 | Coding | 4 | 2126 | cactgtttttaattcatcag | 65 | 64 |
| 224198 | Coding | 4 | 2457 | ataatgttccaattcctact | 31 | 65 |
| 224199 | Stop Codon | 4 | 2735 | agaaaaagctcagttaactt | 57 | 66 |
| 224200 | 3'UTR | 4 | 2828 | attgtagccaggcttctaaa | 68 | 67 |
| 224201 | 3'UTR | 4 | 3056 | atcttcttaaaaataattcg | 18 | 68 |
| 224202 | 3'UTR | 4 | 3193 | tgtgcaattgtggctaccac | 76 | 69 |
| 224203 | 3'UTR | 4 | 3316 | aacaatgtcatgttccaggt | 88 | 70 |
| 224204 | 3'UTR | 4 | 3486 | gctggcaaagtgactataga | 72 | 71 |
| 224205 | 3'UTR | 4 | 3896 | ttccacagaagatgtttatt | 30 | 72 |
| 224206 | 3'UTR | 4 | 3899 | tttttccacagaagatgttt | 14 | 73 |
| 224207 | intron | 11 | 11258 | tagagctaaacgatctagaa | 47 | 74 |
| 224208 | intron | 11 | 23630 | taactctttctggccttgaa | 93 | 75 |
| 224209 | intron | 11 | 25682 | attggccctaacagaaaatc | 19 | 76 |
| 224210 | intron: exon junction | 11 | 27616 | agaacttatcctacttaaca | 7 | 77 |
| 224211 | intron | 11 | 39357 | gtttccctcgtgttgctcag | 63 | 78 |
| 224212 | exon: intron junction | 11 | 39759 | ttgtacttactatcatgatg | 25 | 79 |
| 224213 | exon: intron junction | 11 | 41520 | acttacttacctcacaacgt | 9 | 80 |
| 224214 | intron: exon junction | 11 | 47989 | aatctgtgtcctttaaaaca | 35 | 81 |
| 224215 | exon | 11 | 2745 | tgtgcactgaggagctgagg | 19 | 82 |
| 224216 | exon | 4 | 296 | acgttcagaacttatctttt | 45 | 83 |
| 224217 | Stop Codon | 13 | 2221 | catgctaaataattcctact | 0 | 84 |

**[0205]** As shown in Table 1, SEQ ID NOs 14, 15, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31, 32, 35, 36, 40, 41, 42, 43, 44, 45, 47, 48, 49, 50, 51, 53, 55, 57, 58, 59, 60, 61, 63, 64, 66, 67, 69, 70, 71, 74, 75, 78 and 83 demonstrated at least 40% inhibition of human HIF1α expression in this assay and are therefore preferred. More preferred are SEQ ID NOs 47, 48 and 25. The target regions to which these preferred sequences are complementary are

herein referred to as "preferred target segments" and are therefore preferred for targeting by compounds of the present invention. These preferred target segments are shown in Table 2. The sequences represent the reverse complement of the preferred antisense compounds shown in Table 1. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 2 is the species in which each of the preferred target segments was found.

**Table 2**
**Sequence and position of preferred target segments identified in HIF1α.**

| SITE ID | TARGET SEQ ID NO | TARGET SITE | SEQUENCE | REV COMP OF SEQ ID | ACTIVE IN | SEQ ID NO |
|---|---|---|---|---|---|---|
| 90592 | 4 | 2496 | tgcagctactacatcacttt | 14 | *H. sapiens* | 85 |
| 90593 | 4 | 854 | acattcacgtatatgatacc | 15 | *H. sapiens* | 86 |
| 90595 | 4 | 2039 | gcgcaagtcctcaaagcaca | 17 | *H. sapiens* | 87 |
| 90596 | 4 | 583 | ggtgacatgatttacatttc | 18 | *H. sapiens* | 88 |
| 90597 | 4 | 1408 | gatacaagtagcctctttga | 19 | *H. sapiens* | 89 |
| 90598 | 4 | 1674 | caatcaagaagttgcattaa | 20 | *H. sapiens* | 90 |
| 90599 | 4 | 3333 | gttaatcatataataatgat | 21 | *H. sapiens* | 91 |
| 90600 | 4 | 152 | cacctctggacttgcctttc | 22 | *H. sapiens* | 92 |
| 90601 | 4 | 3027 | atttttggctagggagttta | 23 | *H. sapiens* | 93 |
| 90602 | 4 | 2085 | acaagaacctactgctaatg | 24 | *H. sapiens* | 94 |
| 90603 | 4 | 3101 | agtaacctttcatcatgatc | 25 | *H. sapiens* | 95 |
| 90604 | 4 | 1001 | acagcctggatatgaaattt | 26 | *H. sapiens* | 96 |
| 90606 | 4 | 1983 | gttacgttccttcgatcagt | 28 | *H. sapiens* | 97 |
| 90607 | 4 | 2404 | cagaatgctcagagaaagcg | 29 | *H. sapiens* | 98 |
| 90608 | 4 | 649 | ggacacagtgtgtttgattt | 30 | *H. sapiens* | 99 |
| 90609 | 4 | 1139 | atgatatgtttactaaagga | 31 | *H. sapiens* | 100 |
| 90610 | 4 | 1442 | aacctgatgctttaactttg | 32 | *H. sapiens* | 101 |
| 90613 | 4 | 110 | gcttctctctagtctcacga | 35 | *H. sapiens* | 102 |
| 90614 | 4 | 3094 | agaaggcagtaacctttcat | 36 | *H. sapiens* | 103 |
| 90618 | 4 | 350 | ggcgaagtaaagaatctgaa | 40 | *H. sapiens* | 104 |
| 90619 | 4 | 2320 | agaagccctaacgtgttatc | 41 | *H. sapiens* | 105 |
| 90620 | 4 | 2331 | cgtgttatctgtcgctttga | 42 | *H. sapiens* | 106 |
| 90621 | 4 | 1091 | atgaatattatcatgctttg | 43 | *H. sapiens* | 107 |
| 90622 | 4 | 565 | atggttctcacagatgatgg | 44 | *H. sapiens* | 108 |
| 90623 | 4 | 2222 | gtgccacatcatcaccatat | 45 | *H. sapiens* | 109 |
| 90625 | 4 | 2931 | gctggatcacagacagctca | 47 | *H. sapiens* | 110 |
| 90626 | 4 | 2321 | gaagccctaacgtgttatct | 48 | *H. sapiens* | 111 |
| 90627 | 4 | 248 | gcggggaccgattcaccatg | 49 | *H. sapiens* | 112 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 90628 | 4 | 1224 | agcaactgtcatatataaca | 50 | *H. sapiens* | 113 |
| 140838 | 4 | 414 | gagttcgcatcttgataagg | 51 | *H. sapiens* | 114 |
| 140840 | 4 | 619 | tacatgggattaactcagtt | 53 | *H. sapiens* | 115 |
| 140842 | 4 | 706 | cttacacacagaaatggcct | 55 | *H. sapiens* | 116 |
| 140844 | 4 | 1036 | agaattaccgaattgatggg | 57 | *H. sapiens* | 117 |
| 140845 | 4 | 1125 | gaccaaaactcatcatgata | 58 | *H. sapiens* | 118 |
| 140846 | 4 | 1283 | acgttgtgagtggtattatt | 59 | *H. sapiens* | 119 |
| 140847 | 4 | 1380 | tcagctattcaccaaagttg | 60 | *H. sapiens* | 120 |
| 140848 | 4 | 1699 | gaaccaaatccagagtcact | 61 | *H. sapiens* | 121 |
| 140850 | 4 | 1995 | cgatcagttgtcaccattag | 63 | *H. sapiens* | 122 |
| 140851 | 4 | 2126 | ctgatgaattaaaaacagtg | 64 | *H. sapiens* | 123 |
| 140853 | 4 | 2735 | aagttaactgagctttttct | 66 | *H. sapiens* | 124 |
| 140854 | 4 | 2828 | tttagaagcctggctacaat | 67 | *H. sapiens* | 125 |
| 140856 | 4 | 3193 | gtggtagccacaattgcaca | 69 | *H. sapiens* | 126 |
| 140857 | 4 | 3316 | acctggaacatgacattgtt | 70 | *H. sapiens* | 127 |
| 140858 | 4 | 3486 | tctatagtcactttgccagc | 71 | *H. sapiens* | 128 |
| 140861 | 11 | 11258 | ttctagatcgtttagctcta | 74 | *H. sapiens* | 129 |
| 140862 | 11 | 23630 | ttcaaggccagaaagagtta | 75 | *H. sapiens* | 130 |
| 140865 | 11 | 39357 | ctgagcaacacgagggaaac | 78 | *H. sapiens* | 131 |
| 140870 | 4 | 296 | aaaagataagttctgaacgt | 83 | *H. sapiens* | 132 |

**[0206]** As these "preferred target segments" have been found by experimentation to be open to, and accessible for, hybridization with the antisense compounds of the present invention, one of skill in the art will recognize or be able to ascertain, using no more than routine experimentation, further embodiments of the invention that encompass other compounds that specifically hybridize to these preferred target segments and consequently inhibit the expression of HIF1α.

**[0207]** According to the present invention, antisense compounds include antisense oligomeric compounds, antisense oligonucleotides, ribozymes, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and other short oligomeric compounds which hybridize to at least a portion of the target nucleic acid.

**Exampl 16**

**Western blot analysis of HIF1α or HIF2α prot in levels**

**[0208]** Western blot analysis (immunoblot analysis) is carried out using standard methods. Cells are harvested 16-20 h after oligonucleotide treatment, washed once with PBS, suspended in Laemmli buffer (100 ul/well), boiled for 5 minutes and loaded on a 16% SDS-PAGE gel. Gels are run for 1.5 hours at 150 V, and transferred to membrane for western blotting. Appropriate primary antibody directed to HIF1α or HIF2α is used, with a radiolabeled or fluorescently labeled secondary antibody directed against the primary antibody species. Bands are visualized using a PHOSPHORIMAGER™ (Molecular Dynamics, Sunnyvale CA).

**Example 17**

**Additional antisense oligonucleotides against human HIF1α**

**[0209]** A series of antisense compounds were designed to target different regions of the human HIF1α RNA, using published sequences (GenBank accession number U29165.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 133). The compounds are shown in Table 3. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 3 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on human HIF1α mRNA levels by quantitative real-time

PCR as described in other examples herein. Data are averages from three experiments in which A549 cells were treated with the antisense oligonucleotides of the present invention. "Species" indicates the animal species of HIF1α nucleic acid to which the compounds are fully complementary (H = human, M = mouse, R = rat). As noted many of the compounds are fully complementary to more than one species.

**Table 3**

**Inhibition of human HIF1α mRNA levels by additional chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

| ISIS # | REGION | TARGET seq id no | TARGET site | Sequence | % INHIB | SEQ ID NO | Species |
|---|---|---|---|---|---|---|---|
| 298690 | Coding | 133 | 373 | tgatgagcaagctcataaaa | 51 | 134 | H,M,R |
| 298691 | Coding | 133 | 378 | gcaactgatgagcaagctca | 77 | 135 | H,M,R |
| 298692 | Coding | 133 | 385 | ggaagtggcaactgatgagc | 62 | 136 | H,M,R |
| 298693 | Coding | 133 | 631 | ccagttagttcaaactgagt | 79 | 137 | H,M,R |
| 298694 | Coding | 133 | 636 | tgtgtccagttagttcaaac | 79 | 138 | H,M,R |
| 298695 | Coding | 133 | 641 | cacactgtgtccagttagtt | 79 | 139 | H,M,R |
| 298696 | Coding | 133 | 663 | cacatggatgagtaaaatca | 69 | 140 | H,M |
| 298697 | Coding | 133 | 673 | tcctcatggtcacatggatg | 84 | 141 | H,M,R |
| 298698 | Coding | 133 | 682 | tctctcatttcctcatggtc | 80 | 142 | H,M,R |
| 298699 | Coding | 133 | 687 | gcatttctctcatttcctca | 73 | 143 | H,M,R |
| 298700 | Coding | 133 | 695 | gtgtgtaagcatttctctca | 67 | 144 | H,M,R |
| 298701 | Coding | 133 | 705 | ggccatttctgtgtgtaagc | 78 | 145 | H,M,R |
| 298702 | Coding | 133 | 865 | tggttactgttggtatcata | 85 | 146 | H,M |
| 298703 | Coding | 133 | 919 | tcacaaatcagcaccaagca | 57 | 147 | H,M,R |
| 298704 | Coding | 133 | 924 | tgggttcacaaatcagcacc | 71 | 148 | H,M,R |
| 298705 | Coding | 133 | 931 | tgaggaatgggttcacaaat | 69 | 149 | H,M,R |
| 298706 | Coding | 133 | 967 | gtcttgctatctaaaggaat | 58 | 150 | H,M |
| 298707 | Coding | 133 | 1078 | tattcataaattgagcggcc | 80 | 151 | H,M |
| 298708 | Coding | 133 | 1084 | tgataatattcataaattga | 13 | 152 | H,M,R |
| 298709 | Coding | 133 | 1117 | tgagttttggtcagatgatc | 64 | 153 | H,M,R |
| 298710 | Coding | 133 | 1144 | acttgtcctttagtaaacat | 58 | 154 | H,M,R |
| 298711 | Coding | 133 | 1149 | tggtgacttgtcctttagta | 75 | 155 | H,M,R |
| 298712 | Coding | 133 | 1154 | tcctgtggtgacttgtcctt | 76 | 156 | H,M,R |
| 298713 | Coding | 133 | 1159 | tactgtcctgtggtgacttg | 62 | 157 | H,M,R |
| 298714 | Coding | 133 | 1164 | tcctgtactgtcctgtggtg | 83 | 158 | H,M,R |
| 298715 | Coding | 133 | 1171 | gcaagcatcctgtactgtcc | 67 | 159 | H,M,R |
| 298716 | Coding | 133 | 1192 | cagacatatccacctctttt | 56 | 160 | H,M,R |
| 298717 | Coding | 133 | 1198 | tcaacccagacatatccacc | 53 | 161 | H,M,R |
| 298718 | Coding | 133 | 1217 | tatgacagttgcttgagttt | 64 | 162 | H,M |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 298719 | Coding | 133 | 1222 | ttatatatgacagttgcttg | 69 | 163 | H,M |
| 298720 | Coding | 133 | 1308 | gaagggagaaaatcaagtcg | 46 | 164 | H,M,R |
| 298721 | Coding | 133 | 1320 | attctgtttgttgaagggag | 43 | 165 | H,M,R |
| 298722 | Coding | 133 | 1354 | ttcatatctgaagattcaac | 53 | 166 | H,M,R |
| 298723 | Coding | 133 | 1387 | tctgattcaactttggtgaa | 59 | 167 | H,M |
| 298724 | Coding | 133 | 1549 | attacatcattatataatgg | 39 | 168 | H,M |
| 298725 | Coding | 133 | 1639 | ctacttcgaagtggctttgg | 77 | 169 | H,M,R |
| 298726 | Coding | 133 | 1645 | tcagcactacttcgaagtgg | 80 | 170 | H,M,R |
| 298727 | Coding | 133 | 1771 | ctttgtctagtgcttccatc | 73 | 171 | H,M,R |
| 298728 | Coding | 133 | 1955 | atcatccattgggatatagg | 74 | 172 | H,M,R |
| 298729 | Coding | 133 | 1996 | tctaatggtgacaactgatc | 78 | 173 | H,M,R |
| 298730 | Coding | 133 | 2421 | catcatgttccatttttcgc | 69 | 174 | H,M,R |
| 298731 | Coding | 133 | 2632 | gtcagctgtggtaatccact | 69 | 175 | H,M,R |
| 298732 | Coding | 133 | 2638 | taactggtcagctgtggtaa | 58 | 176 | H,M,R |
| 298733 | Coding | 133 | 2659 | ggagcattaacttcacaatc | 39 | 177 | H,M,R |
| 298734 | Coding | 133 | 2680 | aggtttctgctgccttgtat | 65 | 178 | H,M,R |
| 298735 | Coding | 133 | 2689 | ccctgcagtaggtttctgct | 63 | 179 | H,M,R |
| 298736 | Coding | 133 | 2694 | cttcaccctgcagtaggttt | 76 | 180 | H,M,R |
| 298737 | Coding | 133 | 2699 | taattcttcaccctgcagta | 71 | 181 | H,M,R |
| 298738 | Coding | 133 | 2704 | ctgagtaattcttcaccctg | 77 | 182 | H,M,R |
| 298739 | Coding | 133 | 2709 | aagctctgagtaattcttca | 84 | 183 | H,M,R |
| 298740 | Coding | 133 | 2714 | atccaaagctctgagtaatt | 66 | 184 | H,M,R |
| 298741 | Coding | 133 | 2719 | acttgatccaaagctctgag | 72 | 185 | H,M,R |
| 298742 | Stop codon | 133 | 2728 | gctcagttaacttgatccaa | 80 | 186 | H,M,R |
| 298743 | 3' UTR | 133 | 2770 | tgagccaccagtgtccaaaa | 85 | 187 | H,M,R |
| 298744 | 3' UTR | 133 | 2821 | ccaggcttctaaaattagat | 68 | 188 | H,M |
| 298745 | 3' UTR | 133 | 2835 | gtgcagtattgtagccaggc | 78 | 189 | H,M |
| 298746 | 3' UTR | 133 | 2840 | agtttgtgcagtattgtagc | 74 | 190 | H,M |
| 298747 | 3' UTR | 133 | 3004 | taaataaaaaggtgcatttt | 0 | 191 | H,M,R |
| 298749 | 3' UTR | 133 | 3110 | actgcctatgatcatgatga | 74 | 192 | H,M |
| 298750 | 3' UTR | 133 | 3194 | ttgtgcaattgtggctacca | 79 | 193 | H,M,R |
| 298751 | 3' UTR | 133 | 3199 | atatattgtgcaattgtggc | 0 | 194 | H,M,R |
| 298752 | 3' UTR | 133 | 3204 | agaaaatatattgtgcaatt | 31 | 195 | H,M,R |
| 298753 | 3' UTR | 133 | 3264 | cttaaaaactagttttataa | 21 | 196 | H,M,R |
| 298754 | 3' UTR | 133 | 3382 | atgtaaatggctttacccat | 68 | 197 | H,M,R |
| 298755 | 3' UTR | 133 | 3437 | ttttatccaaataaatgcca | 59 | 198 | H,M,R |
| 298756 | 3' UTR | 133 | 3443 | tgagaattttatccaaataa | 44 | 199 | H,M,R |
| 298757 | 3' UTR | 133 | 3701 | taatagcgacaaagtgcata | 81 | 200 | H,M,R |
| 298758 | 3' UTR | 133 | 3706 | gatgttaatagcgacaaagt | 54 | 201 | H,M,R |
| 298759 | 3' UTR | 133 | 3711 | aaaaggatgttaatagcgac | 77 | 202 | H,M,R |
| 298760 | 3' UTR | 133 | 3752 | aatgcttctaaaattactca | 62 | 203 | H,M,R |
| 298761 | 3' UTR | 133 | 3766 | tatattcctaaaataatgct | 30 | 204 | H,M |
| 298762 | 3' UTR | 133 | 3892 | acagaagatgtttatttgat | 44 | 205 | H,M,R |

In Table 3, SEQ ID NO 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 166, 167, 169,

170, 171, 172, 173, 174, 175, 176, 178, 179, 180, 181, 182, 184, 185, 186, 187, 188, 189, 190, 192, 193, 197, 198, 200, 201, 202 and 203 demonstrated at least 50% inhibition of HIF1α expression and are therefore preferred.

**Example 18**

**Antisense inhibition of mouse HIF1α expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

**[0210]** In accordance with the present invention, a series of antisense compounds were designed to target different regions of the mouse HIF1α RNA, using published sequences (GenBank accession number NM_010431.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 206. The compounds are shown in Table 4. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 4 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on mouse HIF1α mRNA levels by quantitative real-time PCR as described in other examples herein. Unlike previous examples, the oligonucleotide concentration in this experiment is 50 nM. Data are averages from three experiments in which b.END cells were treated with the antisense oligonucleotides of the present invention. In Table 4,

"Species" indicates the animal species of HIF1α nucleic acid to which the compounds are fully complementary (H = human, M = mouse, R = rat). As noted many of the compounds are fully complementary to more than one species.

**Table 4**

**Inhibition of mouse HIF1α mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

| ISIS # | REGION | TARGET SEQ ID | TARGET SITE | Sequence | % INHIB | SEQ ID NO | Species |
|---|---|---|---|---|---|---|---|
| 298690 | Coding | 206 | 366 | tgatgagcaagctcataaaa | 32 | 134 | H, M, R |
| 298691 | Coding | 206 | 371 | gcaactgatgagcaagctca | 67 | 135 | H, M, R |
| 298692 | Coding | 206 | 378 | ggaagtggcaactgatgagc | 33 | 136 | H, M, R |
| 298693 | Coding | 206 | 624 | ccagttagttcaaactgagt | 58 | 137 | H, M, R |
| 298694 | Coding | 206 | 629 | tgtgtccagttagttcaaac | 39 | 138 | H, M, R |
| 298695 | Coding | 206 | 634 | cacactgtgtccagttagtt | 71 | 139 | H, M, R |
| 298696 | Coding | 206 | 656 | cacatggatgagtaaaatca | 60 | 140 | H, M |
| 298697 | Coding | 206 | 666 | tcctcatggtcacatggatg | 56 | 141 | H, M, R |
| 298698 | Coding | 206 | 675 | tctctcatttcctcatggtc | 69 | 142 | H, M, R |
| 298699 | Coding | 206 | 680 | gcatttctctcatttcctca | 70 | 143 | H, M, R |
| 298700 | Coding | 206 | 688 | gtgtgtaagcatttctctca | 64 | 144 | H, M, R |
| 298701 | Coding | 206 | 698 | ggccatttctgtgtgtaagc | 46 | 145 | H, M, R |
| 298702 | Coding | 206 | 858 | tggttactgttggtatcata | 69 | 146 | H, M |
| 298703 | Coding | 206 | 912 | tcacaaatcagcaccaagca | 45 | 147 | H, M, R |
| 298704 | Coding | 206 | 917 | tgggttcacaaatcagcacc | 34 | 148 | H, M, R |
| 298705 | Coding | 206 | 924 | tgaggaatgggttcacaaat | 64 | 149 | H, M, R |
| 298706 | Coding | 206 | 960 | gtcttgctatctaaaggaat | 42 | 150 | H, M |
| 298707 | Coding | 206 | 1071 | tattcataaattgagcggcc | 64 | 151 | H, M |
| 298708 | Coding | 206 | 1077 | tgataatattcataaattga | 0 | 152 | H, M, R |
| 298709 | Coding | 206 | 1110 | tgagttttggtcagatgatc | 26 | 153 | H, M, R |
| 298710 | Coding | 206 | 1137 | acttgtcctttagtaaacat | 47 | 154 | H, M, R |
| 298711 | Coding | 206 | 1142 | tggtgacttgtcctttagta | 64 | 155 | H, M, R |
| 298712 | Coding | 206 | 1147 | tcctgtggtgacttgtcctt | 58 | 156 | H, M, R |
| 298713 | Coding | 206 | 1152 | tactgtcctgtggtgacttg | 48 | 157 | H, M, R |
| 298714 | Coding | 206 | 1157 | tcctgtactgtcctgtggtg | 61 | 158 | H, M, R |
| 298715 | Coding | 206 | 1164 | gcaagcatcctgtactgtcc | 70 | 159 | H, M, R |
| 298716 | Coding | 206 | 1185 | cagacatatccacctctttt | 43 | 160 | H, M, R |
| 298717 | Coding | 206 | 1191 | tcaacccagacatatccacc | 55 | 161 | H, M, R |
| 298718 | Coding | 206 | 1210 | tatgacagttgcttgagttt | 39 | 162 | H, M |
| 298719 | Coding | 206 | 1215 | ttatatatgacagttgcttg | 42 | 163 | H, M |
| 298720 | Coding | 206 | 1301 | gaagggagaaaatcaagtcg | 23 | 164 | H, M, R |
| 298721 | Coding | 206 | 1313 | attctgtttgttgaagggag | 30 | 165 | H, M, R |
| 298722 | Coding | 206 | 1347 | ttcatatctgaagattcaac | 5 | 166 | H, M, R |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 298723 | Coding | 206 | 1380 | tctgattcaactttggtgaa | 52 | 167 | H, M |
| 298724 | Coding | 206 | 1542 | attacatcattatataatgg | 29 | 168 | H, M |
| 298725 | Coding | 206 | 1629 | ctacttcgaagtggctttgg | 57 | 169 | H, M, R |
| 298726 | Coding | 206 | 1635 | tcagcactacttcgaagtgg | 59 | 170 | H, M, R |
| 298727 | Coding | 206 | 1761 | ctttgtctagtgcttccatc | 46 | 171 | H, M, R |
| 298728 | Coding | 206 | 1987 | atcatccattgggatatagg | 29 | 172 | H, M, R |
| 298729 | Coding | 206 | 2028 | tctaatggtgacaactgatc | 19 | 173 | H, M, R |
| 298730 | Coding | 206 | 2444 | catcatgttccatttttcgc | 55 | 174 | H, M, R |
| 298731 | Coding | 206 | 2655 | gtcagctgtggtaatccact | 59 | 175 | H, M, R |
| 298732 | Coding | 206 | 2661 | taactggtcagctgtggtaa | 62 | 176 | H, M, R |
| 298733 | Coding | 206 | 2682 | ggagcattaacttcacaatc | 32 | 177 | H, M, R |
| 298734 | Coding | 206 | 2703 | aggtttctgctgccttgtat | 50 | 178 | H, M, R |
| 298735 | Coding | 206 | 2712 | ccctgcagtaggtttctgct | 53 | 179 | H, M, R |
| 298736 | Coding | 206 | 2717 | cttcaccctgcagtaggttt | 46 | 180 | H, M, R |
| 298737 | Coding | 206 | 2722 | taattcttcaccctgcagta | 42 | 181 | H, M, R |
| 298738 | Coding | 206 | 2727 | ctgagtaattcttcaccctg | 62 | 182 | H, M, R |
| 298739 | Coding | 206 | 2732 | aagctctgagtaattcttca | 44 | 183 | H, M, R |
| 298740 | Coding | 206 | 2737 | atccaaagctctgagtaatt | 42 | 184 | H, M, R |
| 298741 | Coding | 206 | 2742 | acttgatccaaagctctgag | 47 | 185 | H, M, R |
| 298742 | Stop codon | 206 | 2751 | gctcagttaacttgatccaa | 67 | 186 | H, M, R |
| 298743 | 3' UTR | 206 | 2853 | tgagccaccagtgtccaaaa | 56 | 187 | H, M, R |
| 298744 | 3' UTR | 206 | 2895 | ccaggcttctaaaattagat | 48 | 188 | H, M |
| 298745 | 3' UTR | 206 | 2909 | gtgcagtattgtagccaggc | 72 | 189 | H, M |
| 298746 | 3' UTR | 206 | 2914 | agtttgtgcagtattgtagc | 62 | 190 | H, M |
| 298747 | 3' UTR | 206 | 3067 | taaataaaaaggtgcatttt | 4 | 191 | H, M, R |
| 298748 | 3' UTR | 206 | 3162 | gatcatgatgagaatttact | 56 | 207 | M |
| 298749 | 3' UTR | 206 | 3171 | actgcctatgatcatgatga | 64 | 192 | H, M, |
| 298750 | 3' UTR | 206 | 3253 | ttgtgcaattgtggctacca | 74 | 193 | H, M, R |
| 298751 | 3' UTR | 206 | 3258 | atatattgtgcaattgtggc | 67 | 194 | H, M, R |
| 298752 | 3' UTR | 206 | 3263 | agaaaatatattgtgcaatt | 24 | 195 | H, M, R |
| 298753 | 3' UTR | 206 | 3322 | cttaaaaactagttttataa | 0 | 196 | H, M, R |
| 298754 | 3' UTR | 206 | 3428 | atgtaaatggctttacccat | 51 | 197 | H, M, R |
| 298755 | 3' UTR | 206 | 3483 | ttttatccaaataaatgcca | 28 | 198 | H, M, R |
| 298756 | 3' UTR | 206 | 3489 | tgagaattttatccaaataa | 14 | 199 | H, M, R |
| 298757 | 3' UTR | 206 | 3739 | taatagcgacaaagtgcata | 43 | 200 | H, M, R |
| 298758 | 3' UTR | 206 | 3744 | gatgttaatagcgacaaagt | 23 | 201 | H, M, R |
| 298759 | 3' UTR | 206 | 3749 | aaaaggatgttaatagcgac | 45 | 202 | H, M, R |
| 298760 | 3' UTR | 206 | 3789 | aatgcttctaaaattactca | 30 | 203 | H, M, R |
| 298761 | 3' UTR | 206 | 3803 | tatattcctaaaataatgct | 0 | 204 | H, M |
| 298762 | 3' UTR | 206 | 3928 | acagaagatgtttatttgat | 21 | 205 | H, M, R |

In Table 4, SEQ ID NOs 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 167, 169, 170, 171, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 207, 192, 193, 194, 197, 200,

and 202 demonstrated at least 32% inhibition of HIF1α expression and are therefore preferred.

**Example 19**

**Real-time Quantitative PCR Analysis of HIF2α mRNA Levels**

**[0211]** Quantitation of HIF2α mRNA levels was accomplished by real-time quantitative PCR using the ABI PRISM™ 7600, 7700, or 7900 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) as described in previous examples.

**[0212]** Probes and primers to human HIF2α were designed to hybridize to a human HIF2α sequence, using published sequence information (GenBank accession number NM_001430.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 208). For human HIF2α the PCR primers were:
forward primer: AAGCCTTGGAGGGTTTCATTG (SEQ ID NO: 209)
reverse primer: TGCTGATGTTTTCTGACAGAAAGAT (SEQ ID NO: 210)
and the PCR probe was: FAM-CGTGGTGACCCAAGATGGCGACA-TAMRA (SEQ ID NO: 211) where FAM is the fluorescent dye and TAMRA is the quencher dye. For human GAPDH the PCR primers and probe were those listed in previous examples (SEQ ID NOs: 8, 9, 10).

**[0213]** Probes and primers to mouse HIF2α were designed to hybridize to a mouse HIF2α sequence, using published sequence information (GenBank accession number NM_010137.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 212). For mouse HIF2α the PCR primers were:
forward primer: GGCCATCGTTCGAGCCTTA (SEQ ID NO: 213)
reverse primer: GGCACGGGCACGTTCA (SEQ ID NO: 214) and the PCR probe was: FAM-CTGTTGCCGGAACTGACCAGATATGACTG-TAMRA (SEQ ID NO: 215) where FAM is the fluorescent reporter dye

and TAMRA is the quencher dye. For mouse GAPDH the PCR primers were:
forward primer: GGCAAATTCAACGGCACAGT(SEQ ID NO: 216)
reverse primer: GGGTCTCGCTCCTGGAAGAT(SEQ ID NO: 217) and the PCR probe was: 5' JOE-AAGGCCGAGAATGGGAAGCTTGTCATC- TAMRA 3' (SEQ ID NO: 218) where JOE is the fluorescent reporter dye and TAMRA is the quencher dye.

**Example 20**

**Northern blot analysis of HIF2α mRNA levels**

**[0214]** Eighteen hours after antisense treatment, cell monolayers were washed twice with cold PBS and lysed in 1 mL RNAZOL™ (TEL-TEST "B" Inc., Friendswood, TX). Total RNA was prepared following manufacturer's recommended protocols. Electrophoresis and blotting was performed as described in previous examples.

**[0215]** To detect human HIF2α, a human HIF2α specific probe was prepared by PCR using the forward primer AAGCCTTGGAGGGTTTCATTG (SEQ ID NO: 209) and the reverse primer TGCTGATGTTTTCTGACAGAAAGAT (SEQ ID NO: 210). To normalize for variations in loading and transfer efficiency membranes were stripped and probed for human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

**[0216]** To detect mouse HIF2α, a mouse HIF2α specific probe was prepared by PCR using the forward primer GGCCATCGTTCGAGCCTTA (ID NO: 213) and the reverse primer GGCACGGGCACGTTCA (SEQ ID NO: 214). To normalize for variations in loading and
transfer efficiency membranes were stripped and probed for mouse glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RNA (Clontech, Palo Alto, CA).

**Example 21**

**Antisense inhibition of human HIF2α expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

**[0217]** In accordance with the present invention, a series of antisense compounds were designed to target different regions of the human HIF2α RNA, using published sequences (GenBank accession number NM_001430.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 208). The compounds are shown in Table 5. "Target site" indicates the first (5'-most) nucleotide number on the particular target sequence to which the compound binds. All compounds in Table 5 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten 2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on human HIF2α mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from three experiments in which A549 cells were treated with the antisense oligonucleotides of the present invention.

**Table 5**

**Inhibition of human HIF2α mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

| ISIS # | REGION | TARGET SEQ ID NO | TARGET SITE | SEQUENCE | % INHIB | SEQ ID NO |
|---|---|---|---|---|---|---|

| | | | | | | |
|---|---|---|---|---|---|---|
| 221985 | Start Codon | 208 | 142 | gtcagctgtcattgtcgctg | 74 | 219 |
| 221987 | Stop Codon | 208 | 2751 | ggcctggctcaggtggcctg | 54 | 220 |
| 221989 | Coding | 208 | 1000 | ggtcatgttctcggagtcta | 82 | 221 |
| 221991 | Coding | 208 | 1572 | gtggagcagctgctgctgct | 80 | 222 |
| 221993 | Coding | 208 | 2412 | ggtacatttgcgctcagtgg | 76 | 223 |
| 221995 | Coding | 208 | 2206 | tgggcctcgagccccaaaac | 15 | 224 |
| 221997 | Coding | 208 | 1300 | gaataggaagttactcttct | 51 | 225 |
| 221999 | Coding | 208 | 1752 | tggaagtcttccccgtccat | 69 | 226 |
| 222001 | Coding | 208 | 947 | gcagctcctcagggtggtaa | 82 | 227 |
| 222003 | Coding | 208 | 977 | catggtagaattcataggct | 82 | 228 |
| 222005 | Coding | 208 | 1631 | tcacttcaatcttcaggtcg | 55 | 229 |
| 222007 | Coding | 208 | 2691 | gagcttcccagcacgggcac | 79 | 230 |
| 222009 | Coding | 208 | 1502 | tgaaggcaggcaggctccca | 77 | 231 |
| 222011 | Coding | 208 | 2008 | ggtgctggcctggccacagc | 72 | 232 |
| 222013 | Coding | 208 | 561 | cgaatctcctcatggtcgca | 89 | 233 |
| 222015 | Coding | 208 | 1247 | tgctgttcatggccatcagg | 78 | 234 |
| 222017 | Coding | 208 | 1679 | tactgcattggtccttggcc | 78 | 235 |
| 222019 | Coding | 208 | 1488 | ctcccagcctcgctctgggt | 63 | 236 |
| 222021 | Coding | 208 | 2700 | aggagcgtggagcttcccag | 59 | 237 |
| 222023 | Coding | 208 | 623 | ctgtggacatgtctttgctt | 79 | 238 |
| 222025 | Coding | 208 | 1716 | agtgtctccaagtccagctc | 84 | 239 |
| 222027 | Coding | 208 | 759 | ctattgtgaggagggcagtt | 75 | 240 |
| 222029 | Coding | 208 | 237 | tcatagaacacctccgtctc | 37 | 241 |
| 222031 | Coding | 208 | 2334 | aaatgtgaggtgctgccacc | 67 | 242 |
| 222033 | Coding | 208 | 1578 | ttgggcgtggagcagctgct | 54 | 243 |
| 222035 | Coding | 208 | 2126 | gcgctgctcccaagaactct | 89 | 244 |
| 222037 | Coding | 208 | 2639 | gcagcaggtaggactcaaat | 64 | 245 |
| 222039 | Coding | 208 | 2325 | gtgctgccaccaggtgggtc | 79 | 246 |
| 222041 | Coding | 208 | 1001 | tggtcatgttctcggagtct | 82 | 247 |
| 222043 | Coding | 208 | 1209 | tcagtctggtccatggagaa | 80 | 248 |
| 222045 | Coding | 208 | 566 | tctcacgaatctcctcatgg | 68 | 249 |
| 222047 | Coding | 208 | 1622 | tcttcaggtcgttatccaaa | 56 | 250 |
| 222049 | Coding | 208 | 2715 | aggtcccctccttgcaggag | 66 | 251 |
| 222051 | Coding | 208 | 246 | tgggccagctcatagaacac | 82 | 252 |
| 222053 | Coding | 208 | 2336 | tcaaatgtgaggtgctgcca | 73 | 253 |
| 222055 | Coding | 208 | 391 | catctgctggtcagcttcgg | 85 | 254 |
| 222057 | Coding | 208 | 1217 | acagggattcagtctggtcc | 84 | 255 |

As shown in Table 5, SEQ ID NOs 219, 220, 221, 211, 223, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254 and 255 demonstrated at least 40% inhibition of HIF2α expression and are therefore preferred. More preferred are SEQ ID NOs 233, 239 and 244. The target regions to which these preferred sequences are complementary are herein referred to as "preferred target segments" and are therefore preferred for targeting by compounds of the present

invention. These preferred target segments are shown in Table 7. These sequences are shown to contain thymine (T) but one of skill in the art will appreciate that thymine (T) is generally replaced by uracil (U) in RNA sequences. The sequences represent the reverse complement of the preferred antisense compounds shown in Table 5. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 7 is the species in which each of the preferred target segments was found.

**Example 22**

**Antisense inhibition of mouse HIF2α expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap.**

**[0218]** In accordance with the present invention, a second series of antisense compounds were designed to target different regions of the mouse HIF2α RNA, using published sequences (GenBank accession number NM_010137.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 212, nucleotides 20468925 to 20547619 of the sequence with GenBank accession number NW_000133.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 257, GenBank accession number BY229956.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 258, and GenBank accession number AK087208.1, incorporated herein by reference and incorporated herein as SEQ ID NO: 259). The compounds are shown in Table 6. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the compound binds. All compounds in Table 6 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region consisting of ten

2'-deoxynucleotides, which is flanked on both sides (5' and 3' directions) by five-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE)nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. All cytidine residues are 5-methylcytidines. The compounds were analyzed for their effect on mouse HIF2α mRNA levels by quantitative real-time PCR as described in other examples herein. Data are averages from three experiments in which b.END cells were treated with the antisense oligonucleotides of the present invention.

**Table 6**

**Inhibition of mouse HIF2α mRNA levels by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap**

| ISIS # | REGION | TARGET SEQ ID NO: | TARGET SITE | SEQUENCE | % INHIB | SEQ ID NO |
|---|---|---|---|---|---|---|
| 320972 | 5'UTR | 212 | 130 | ggttccttaaccccgtaggg | 70 | 260 |
| 320973 | 5'UTR | 212 | 135 | acctgggttccttaaccccg | 61 | 261 |
| 320974 | 5'UTR | 212 | 140 | ggagcacctgggttccttaa | 70 | 262 |
| 320975 | Start Codon | 212 | 178 | ttgtcagctgtcattgtcgc | 72 | 263 |
| 320976 | Start Codon | 212 | 183 | tctccttgtcagctgtcatt | 84 | 264 |
| 320977 | Coding | 212 | 266 | gaagacctccgtctccttgc | 83 | 265 |
| 320978 | Coding | 212 | 317 | caggtgggagctcacactgt | 76 | 266 |
| 320979 | Coding | 212 | 352 | aagctgatggccaggcgcat | 64 | 267 |
| 320980 | Coding | 212 | 442 | ttcaggtacaagttatccat | 78 | 268 |
| 320981 | Coding | 212 | 448 | aaggctttcaggtacaagtt | 73 | 269 |
| 320982 | Coding | 212 | 461 | aatgaaaccctccaaggctt | 87 | 270 |
| 320983 | Coding | 212 | 520 | atgaacttgctgatgttttc | 29 | 271 |
| 320984 | Coding | 212 | 525 | gtcccatgaacttgctgatg | 57 | 272 |
| 320985 | Coding | 212 | 535 | acctgggtaagtcccatgaa | 63 | 273 |
| 320986 | Coding | 212 | 545 | tgttagttctacctgggtaa | 62 | 274 |
| 320987 | Coding | 212 | 563 | gtcaaagatgctgtgtcctg | 83 | 275 |
| 320988 | Coding | 212 | 574 | ggatgagtgaagtcaaagat | 50 | 276 |
| 320989 | Coding | 212 | 673 | atgaagaagtcacgctcggt | 63 | 277 |
| 320990 | Coding | 212 | 682 | ttcatcctcatgaagaagtc | 53 | 278 |
| 320991 | Coding | 212 | 687 | tgcacttcatcctcatgaag | 58 | 279 |
| 320992 | Coding | 212 | 714 | tgacagtccggcctctgttg | 52 | 280 |
| 320993 | Coding | 212 | 766 | actctcacttgcccggtgca | 87 | 281 |
| 320994 | Coding | 212 | 776 | gttgttgtagactctcactt | 64 | 282 |
| 320995 | Coding | 212 | 850 | attggctcacacatgatgat | 76 | 283 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 320996 | Coding | 212 | 860 | tgggtgctggattggctcac | 75 | 284 |
| 320997 | Coding | 212 | 913 | atgctgtggcggctcaggaa | 87 | 285 |
| 320998 | Coding | 212 | 970 | gggtggtaaccaatcagttc | 76 | 286 |
| 320999 | Coding | 212 | 1057 | gtgcacaagttctggtgact | 50 | 287 |
| 321000 | Coding | 212 | 1062 | ccttggtgcacaagttctgg | 74 | 288 |
| 321001 | Coding | 212 | 1135 | gtcccctgggtctccagcca | 78 | 289 |
| 321002 | Coding | 212 | 1140 | tgaccgtcccctgggtctcc | 63 | 290 |
| 321003 | Coding | 212 | 1145 | gtagatgaccgtcccctggg | 68 | 291 |
| 321004 | Coding | 212 | 1150 | gggttgtagatgaccgtccc | 62 | 292 |
| 321005 | Coding | 212 | 1191 | catagttgacacacatgata | 37 | 293 |
| 321006 | Coding | 212 | 1234 | tccatggagaacaccacgtc | 76 | 294 |
| 321007 | Coding | 212 | 1239 | tctggtccatggagaacacc | 83 | 295 |
| 321008 | Coding | 212 | 1286 | aaagatgctgttcatggcca | 51 | 296 |
| 321009 | Coding | 212 | 1338 | tggtgaacaggtagttgctc | 64 | 297 |
| 321010 | Coding | 212 | 1363 | agctcctcgggctcctcctt | 83 | 298 |
| 321011 | Coding | 212 | 1454 | ggccttgccataggctgagg | 49 | 299 |
| 321012 | Coding | 212 | 1459 | aggatggccttgccataggc | 53 | 300 |
| 321013 | Coding | 212 | 1612 | ctgctgggcgtggagcagct | 40 | 301 |
| 321014 | Coding | 212 | 1725 | tgaagtccgtctgggtactg | 58 | 302 |
| 321015 | Coding | 212 | 1939 | tccaactgctgcgggtactt | 82 | 303 |
| 321016 | Coding | 212 | 2002 | ttgctcccagcatcaaagaa | 0 | 304 |
| 321017 | Coding | 212 | 2012 | cagggacccttgctcccag | 81 | 305 |
| 321018 | Coding | 212 | 2038 | gtgctggcctggccacagca | 66 | 306 |
| 321019 | Coding | 212 | 2216 | cttgaacatggagacatgag | 65 | 307 |
| 321020 | Coding | 212 | 2226 | cagacctcatcttgaacatg | 72 | 308 |
| 321021 | Coding | 212 | 2231 | ctttgcagacctcatcttga | 73 | 309 |
| 321022 | Coding | 212 | 2296 | ttcagcttgttggacagggc | 51 | 310 |
| 321023 | Coding | 212 | 2376 | gtgaactgctggtgcctgga | 79 | 311 |
| 321024 | Coding | 212 | 2386 | cacatcaagtgtgaactgct | 0 | 312 |
| 321025 | Coding | 212 | 2413 | ccgcccatgaggctcttcat | 70 | 313 |
| 321026 | Coding | 212 | 2423 | aggacaggtcccgcccatga | 85 | 314 |
| 321027 | Coding | 212 | 2433 | caggcatcaaaggacaggtc | 55 | 315 |
| 321028 | Coding | 212 | 2482 | gatttttgggtgaattcatc | 38 | 316 |
| 321029 | Coding | 212 | 2647 | ctggccacgcctgacacctt | 65 | 317 |
| 321030 | Coding | 212 | 2665 | gatggccccagcagtcgact | 64 | 318 |
| 321031 | Coding | 212 | 2670 | cgaacgatggccccagcagt | 48 | 319 |
| 321032 | Coding | 212 | 2680 | aggtaaggctcgaacgatgg | 65 | 320 |
| 321033 | Coding | 212 | 2707 | cagtcatatctggtcagttc | 78 | 321 |
| 321034 | Coding | 212 | 2712 | cctcacagtcatatctggtc | 83 | 322 |
| 321035 | Coding | 212 | 2717 | gttcacctcacagtcatatc | 66 | 323 |
| 321036 | Coding | 212 | 2722 | ggcacgttcacctcacagtc | 81 | 324 |
| 321037 | Coding | 212 | 2727 | gcacgggcacgttcacctca | 90 | 325 |
| 321038 | Coding | 212 | 2758 | tctctcccctgcaggagtgt | 79 | 326 |
| 321039 | Coding | 212 | 2768 | tctgagaaggtctctcccct | 51 | 327 |
| 321040 | Coding | 212 | 2778 | ggtccagagctctgagaagg | 73 | 328 |
| 321041 | Stop Codon | 212 | 2791 | gctcaggtggcctggtccag | 69 | 329 |
| 321042 | Stop Codon | 212 | 2798 | ggccctggctcaggtggcct | 12 | 330 |
| 321043 | 3'UTR | 212 | 3199 | agaacaagaacacttgagtt | 66 | 331 |
| 321044 | intron | 257 | 12633 | aacagttgagacatgacagt | 67 | 332 |
| 321045 | exon:intron junction | 257 | 74580 | tgtcactaacctcatcttga | 45 | 333 |
| 321046 | 5'UTR | 258 | 235 | acaggagtcacttttctggg | 43 | 334 |
| 321047 | 5'UTR | 258 | 82 | catacagtctcaggacactg | 47 | 335 |
| 321048 | Genomic | 259 | 116 | aatctgtccatgaaaagaca | 33 | 336 |

**[0219]** As shown in Table 6, SEQ ID NO, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 305, 306, 307, 308, 309, 310, 311, 313, 314, 315, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 331, 332, 333, 334 and 335 demonstrated at least 40% inhibition of mouse HIF2α expression in this experiment and are therefore preferred. More preferred are SEQ ID NOs 270, 281 and 285. The target regions to which these preferred sequences are complementary are herein referred to as "preferred target segments" and are therefore preferred for targeting by compounds of the present invention. These preferred target segments are shown in Table 7. These sequences are shown to contain thymine (T) but one of skill in the art will appreciate that thymine (T) is generally replaced by uracil (U) in RNA sequences. The sequences represent the reverse complement of the preferred antisense compounds shown in Tables 5 and 6. "Target site" indicates the first (5'-most) nucleotide number on the particular target nucleic acid to which the oligonucleotide binds. Also shown in Table 3 is the species in which each of the preferred target segments was found.

**Table 7**
**Sequence and position of preferred target segments identified in hypoxia-inducible factor 2 alpha.**

| SITE ID | TARGET SEQ ID NO | TARGET SITE | SEQUENCE | REV COMP OF SEQ ID | ACTIVE IN | SEQ ID NO |
|---|---|---|---|---|---|---|

| | | | | | | |
|---|---|---|---|---|---|---|
| 138730 | 208 | 142 | cagcgacaatgacagctgac | 291 | *H. sapiens* | 337 |
| 138731 | 208 | 2751 | caggccacctgagccaggcc | 292 | *H. sapiens* | 338 |
| 138732 | 208 | 1000 | tagactccgagaacatgacc | 293 | *H. sapiens* | 339 |
| 138733 | 208 | 1572 | agcagcagcagctgctccac | 294 | *H. sapiens* | 340 |
| 138734 | 208 | 2412 | ccactgagcgcaaatgtacc | 295 | *H. sapiens* | 341 |
| 138736 | 208 | 1300 | agaagagtaacttcctattc | 297 | *H. sapiens* | 342 |
| 138737 | 208 | 1752 | atggacggggaagacttcca | 298 | *H. sapiens* | 343 |
| 138738 | 208 | 947 | ttaccaccctgaggagctgc | 299 | *H. sapiens* | 344 |
| 138739 | 208 | 977 | agcctatgaattctaccatg | 300 | *H. sapiens* | 345 |
| 138740 | 208 | 1631 | cgacctgaagattgaagtga | 301 | *H. sapiens* | 346 |
| 138741 | 208 | 2691 | gtgcccgtgctgggaagctc | 302 | *H. sapiens* | 347 |
| 138742 | 208 | 1502 | tgggagcctgcctgccttca | 303 | *H. sapiens* | 348 |
| 138743 | 208 | 2008 | gctgtggccaggccagcacc | 304 | *H. sapiens* | 349 |
| 138744 | 208 | 561 | tgcgaccatgaggagattcg | 305 | *H. sapiens* | 350 |
| 138745 | 208 | 1247 | cctgatggccatgaacagca | 306 | *H. sapiens* | 351 |
| 138746 | 208 | 1679 | ggccaaggaccaatgcagta | 307 | *H. sapiens* | 352 |
| 138747 | 208 | 1488 | acccagagcgaggctgggag | 308 | *H. sapiens* | 353 |
| 138748 | 208 | 2700 | ctgggaagctccacgctcct | 309 | *H. sapiens* | 354 |
| 138749 | 208 | 623 | aagcaaagacatgtccacag | 310 | *H. sapiens* | 355 |
| 138750 | 208 | 1716 | gagctggacttggagacact | 311 | *H. sapiens* | 356 |
| 138751 | 208 | 759 | aactgccctcctcacaatag | 312 | *H. sapiens* | 357 |
| 138753 | 208 | 2334 | ggtggcagcacctcacattt | 314 | *H. sapiens* | 358 |
| 138754 | 208 | 1578 | agcagctgctccacgcccaa | 315 | *H. sapiens* | 359 |
| 138755 | 208 | 2126 | agagttcttgggagcagcgc | 316 | *H. sapiens* | 360 |
| 138756 | 208 | 2639 | atttgagtcctacctgctgc | 317 | *H. sapiens* | 361 |
| 138757 | 208 | 2325 | gacccacctggtggcagcac | 318 | *H. sapiens* | 362 |
| 138758 | 208 | 1001 | agactccgagaacatgacca | 319 | *H. sapiens* | 363 |
| 138759 | 208 | 1209 | ttctccatggaccagactga | 320 | *H. sapiens* | 364 |
| 138760 | 208 | 566 | ccatgaggagattcgtgaga | 321 | *H. sapiens* | 365 |
| 138761 | 208 | 1622 | tttggataacgacctgaaga | 322 | *H. sapiens* | 366 |
| 138762 | 208 | 2715 | ctcctgcaaggaggggacct | 323 | *H. sapiens* | 367 |
| 138763 | 208 | 246 | gtgttctatgagctggccca | 324 | *H. sapiens* | 368 |
| 138764 | 208 | 2336 | tggcagcacctcacatttga | 325 | *H. sapiens* | 369 |
| 138765 | 208 | 391 | ccgaagctgaccagcagatg | 326 | *H. sapiens* | 370 |
| 138766 | 208 | 1217 | ggaccagactgaatccctgt | 327 | *H. sapiens* | 371 |
| 237138 | 212 | 130 | ccctacggggttaaggaacc | 332 | *M. musculus* | 372 |
| 237139 | 212 | 135 | cggggttaaggaacccaggt | 333 | *M. musculus* | 373 |
| 237140 | 212 | 140 | ttaaggaacccaggtgctcc | 334 | *M. musculus* | 374 |
| 237141 | 212 | 178 | gcgacaatgacagctgacaa | 335 | *M. musculus* | 375 |
| 237142 | 212 | 183 | aatgacagctgacaaggaga | 336 | *M. musculus* | 376 |
| 237143 | 212 | 266 | gcaaggagacggaggtcttc | 337 | *M. musculus* | 377 |
| 237144 | 212 | 317 | acagtgtgagctcccacctg | 338 | *M. musculus* | 378 |
| 237145 | 212 | 352 | atgcgcctggccatcagctt | 339 | *M. musculus* | 379 |
| 237146 | 212 | 442 | atggataacttgtacctgaa | 340 | *M. musculus* | 380 |
| 237147 | 212 | 448 | aacttgtacctgaaagcctt | 341 | *M. musculus* | 381 |
| 237148 | 212 | 461 | aagccttggagggtttcatt | 342 | *M. musculus* | 382 |
| 237150 | 212 | 525 | catcagcaagttcatgggac | 344 | *M. musculus* | 383 |
| 237151 | 212 | 535 | ttcatgggacttacccaggt | 345 | *M. musculus* | 384 |
| 237152 | 212 | 545 | ttacccaggtagaactaaca | 346 | *M. musculus* | 385 |
| 237153 | 212 | 563 | caggacacagcatctttgac | 347 | *M. musculus* | 386 |
| 237154 | 212 | 574 | atctttgacttcactcatcc | 348 | *M. musculus* | 387 |
| 237155 | 212 | 673 | accgagcgtgacttcttcat | 349 | *M. musculus* | 388 |
| 237156 | 212 | 682 | gacttcttcatgaggatgaa | 350 | *M. musculus* | 389 |
| 237157 | 212 | 687 | cttcatgaggatgaagtgca | 351 | *M. musculus* | 390 |
| 237158 | 212 | 714 | caacagaggccggactgtca | 352 | *M. musculus* | 391 |
| 237159 | 212 | 766 | tgcaccgggcaagtgagagt | 353 | *M. musculus* | 392 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 237160 | 212 | 776 | aagtgagagtctacaacaac | 354 | *M. musculus* | 393 |
| 237161 | 212 | 850 | atcatcatgtgtgagccaat | 355 | *M. musculus* | 394 |
| 237162 | 212 | 860 | gtgagccaatccagcaccca | 356 | *M. musculus* | 395 |
| 237163 | 212 | 913 | ttcctgagccgccacagcat | 357 | *M. musculus* | 396 |
| 237164 | 212 | 970 | gaactgattggttaccaccc | 358 | *M. musculus* | 397 |
| 237165 | 212 | 1057 | agtcaccagaacttgtgcac | 359 | *M. musculus* | 398 |
| 237166 | 212 | 1062 | ccagaacttgtgcaccaagg | 360 | *M. musculus* | 399 |
| 237167 | 212 | 1135 | tggctggagacccaggggac | 361 | *M. musculus* | 400 |
| 237168 | 212 | 1140 | ggagacccaggggacggtca | 362 | *M. musculus* | 401 |
| 237169 | 212 | 1145 | cccaggggacggtcatctac | 363 | *M. musculus* | 402 |
| 237170 | 212 | 1150 | gggacggtcatctacaaccc | 364 | *M. musculus* | 403 |
| 237172 | 212 | 1234 | gacgtggtgttctccatgga | 366 | *M. musculus* | 404 |
| 237173 | 212 | 1239 | ggtgttctccatggaccaga | 367 | *M. musculus* | 405 |
| 237174 | 212 | 1286 | tggccatgaacagcatcttt | 368 | *M. musculus* | 406 |
| 237175 | 212 | 1338 | gagcaactacctgttcacca | 369 | *M. musculus* | 407 |
| 237176 | 212 | 1363 | aaggaggagcccgaggagct | 370 | *M. musculus* | 408 |
| 237177 | 212 | 1454 | cctcagcctatggcaaggcc | 371 | *M. musculus* | 409 |
| 237178 | 212 | 1459 | gcctatggcaaggccatcct | 372 | *M. musculus* | 410 |
| 237179 | 212 | 1612 | agctgctccacgcccagcag | 373 | *M. musculus* | 411 |
| 237180 | 212 | 1725 | cagtacccagacggacttca | 374 | *M. musculus* | 412 |
| 237181 | 212 | 1939 | aagtacccgcagcagttgga | 375 | *M. musculus* | 413 |
| 237183 | 212 | 2012 | ctgggagcaaagggtccctg | 377 | *M. musculus* | 414 |
| 237184 | 212 | 2038 | tgctgtggccaggccagcac | 378 | *M. musculus* | 415 |
| 237185 | 212 | 2216 | ctcatgtctccatgttcaag | 379 | *M. musculus* | 416 |
| 237186 | 212 | 2226 | catgttcaagatgaggtctg | 380 | *M. musculus* | 417 |
| 237187 | 212 | 2231 | tcaagatgaggtctgcaaag | 381 | *M. musculus* | 418 |
| 237188 | 212 | 2296 | gccctgtccaacaagctgaa | 382 | *M. musculus* | 419 |
| 237189 | 212 | 2376 | tccaggcaccagcagttcac | 383 | *M. musculus* | 420 |
| 237191 | 212 | 2413 | atgaagagcctcatgggcgg | 385 | *M. musculus* | 421 |
| 237192 | 212 | 2423 | tcatgggcgggacctgtcct | 386 | *M. musculus* | 422 |
| 237193 | 212 | 2433 | gacctgtcctttgatgcctg | 387 | *M. musculus* | 423 |
| 237195 | 212 | 2647 | aaggtgtcaggcgtggccag | 389 | *M. musculus* | 424 |
| 237196 | 212 | 2665 | agtcgactgctggggccatc | 390 | *M. musculus* | 425 |
| 237197 | 212 | 2670 | actgctggggccatcgttcg | 391 | *M. musculus* | 426 |
| 237198 | 212 | 2680 | ccatcgttcgagccttacct | 392 | *M. musculus* | 427 |
| 237199 | 212 | 2707 | gaactgaccagatatgactg | 393 | *M. musculus* | 428 |
| 237200 | 212 | 2712 | gaccagatatgactgtgagg | 394 | *M. musculus* | 429 |
| 237201 | 212 | 2717 | gatatgactgtgaggtgaac | 395 | *M. musculus* | 430 |
| 237202 | 212 | 2722 | gactgtgaggtgaacgtgcc | 396 | *M. musculus* | 431 |
| 237203 | 212 | 2727 | tgaggtgaacgtgcccgtgc | 397 | *M. musculus* | 432 |
| 237204 | 212 | 2758 | acactcctgcaggggagaga | 398 | *M. musculus* | 433 |
| 237205 | 212 | 2768 | aggggagagaccttctcaga | 399 | *M. musculus* | 434 |
| 237206 | 212 | 2778 | ccttctcagagctctggacc | 400 | *M. musculus* | 435 |
| 237207 | 212 | 2791 | ctggaccaggccacctgagc | 401 | *M. musculus* | 436 |
| 237209 | 212 | 3199 | aactcaagtgttcttgttct | 403 | *M. musculus* | 437 |
| 237210 | 257 | 12633 | actgtcatgtctcaactgtt | 404 | *M. musculus* | 438 |
| 237211 | 257 | 74580 | tcaagatgaggttagtgaca | 405 | *M. musculus* | 439 |
| 237212 | 258 | 235 | cccagaaaagtgactcctgt | 406 | *M. musculus* | 440 |
| 237213 | 258 | 82 | cagtgtcctgagactgtatg | 407 | *M. musculus* | 441 |

**[0220]** As these "preferred target segments" have been found by experimentation to be open to, and accessible

for, hybridization with the antisense compounds of the present invention, one of skill in the art will recognize or be able to ascertain, using no more than routine experimentation, further embodiments of the invention that encompass other compounds that specifically hybridize to these preferred target segments and consequently inhibit the expression of HIF2α.

**[0221]** According to the present invention, antisense compounds include antisense oligomeric compounds, antisense oligonucleotides, ribozymes, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and other short oligomeric compounds which hybridize to at least a portion of the target nucleic acid.

**Example 23**

**Expression of HIF1α and HIF2α in various human cell lines**

**[0222]** U87-MG human glioblastoma, PC-3 human prostate cancer, JEG-3 human choriocarcinoma, HeLa human cervix cancer, SK-N-BE(2) neuroblastoma, MCF-7 human breast cancer, 786-O human clear-cell renal cell carcinoma, Calu-1 human lung cancer, and Hep3B human hepatocellular carcinoma cells were purchased from American Type Culture Collection (ATCC; Manassas, VA) and cultured according to ATCC directions. Human umbilical endothelial cells (HUVEC) were obtained from Cascade Biologics (Portland OR). Hypoxic treatments of cells (0.5-0.8 x $10^6$/60 mm dish or 1-2 x $10^6$/100 mm dish) were performed at 1% $O_2$ in a chamber controlled by ProOx oxygen sensor (BioSpherix, Redfield, NY) for 16 h. To achieve the optimal hypoxic induction, 3 or 6 ml of medium was used for 60 mm and 100 mm dish culture, respectively during incubation. $CoCl_2$ (150 μM) was added to the cells to mimic hypoxic condition in some experiments.

**[0223]** Cultured cells at normoxia, hypoxia, or with $CoCl_2$ were harvested and whole cell lysates prepared with RIPA buffer containing protease inhibitor cocktails (Roche), 0.5 mM sodium orthovanadate, 10 mM β-glycerophophate, 250 ng/ml ubiquitin aldehyde, and 400 nM epoxomicin were separated on 12% SDS-PAGE and transferred to PVDF membranes (Amersham Biosciences). Typically, 35-50 μg of proteins were loaded per lane. Immunoblotting was performed with the following antibodies: anti-HIF-1α (BD Transduction Laboratories) at 1:250 (v/v); anti-HIF-2α (EPAS1) (Santa Cruz Biotechnology Inc) at 1:150; anti-HIF-1β (BD Transduction Laboratories) at 1:1000; anti-VHL (BD Transduction Laboratories) at 1:500; anti-GLUT-1 (Alpha Diagnostic International) at 1:600, and anti-α-tubulin (Sigma) at 1:2000 in 0.05% Tween-20/Tris-buffered saline (T-TBS) blocking buffer containing 5% nonfat skim milk at 4 °C overnight, followed by washing with T-TBS for 30 min. Goat anti-mouse or rabbit IgGs coupled with HRP (BioRad) were used as secondary antibodies at 1:3000. Immunospecific bands were detected by enhanced chemiluminescence plus (ECL-Plus) detection kit (Amersham Biosciences).

**[0224]** Hif1α expression was shown to be increased in hypoxic conditions and in the presence of $CoCl_2$ (which mimics hypoxia) in U87-MG human glioblastoma, PC-3 human prostate cancer, JEG-3 human choriocarcinoma, HeLa human cervix cancer, SK-N-BE(2) neuroblastoma, MCF-7 human breast cancer, Calu-1 human lung cancer, and Hep3B human hepatocellular carcinoma cells but not 786-O human clear-cell renal cell carcinoma cells.

**[0225]** Hif2α expression was shown to be increased in hypoxic (1% $O_2$) conditions and in the presence of $CoCl_2$ in U87-MG human glioblastoma, PC-3 human prostate cancer, JEG-3

human choriocarcinoma, MCF-7 human breast cancer, 786-O human clear-cell renal cell carcinoma, Calu-1 human lung cancer, Hep3B human hepatocellular carcinoma cells and HUVECs.

**Example 24**

**Antisense modulation of HIF1α mRNA expression in cancer cells (dose response)**

**[0226]** HeLa, Hep3B, or U87-MG cells were plated in 96-well plates (8-10,000/well) 16 h prior to transfection. The following antisense oligonucleotides were delivered into cells by lipofectin (3 μg/ ml per 100 nM oligonucleotide) in Opti-Mem media (Invitrogen) at the indicated concentration: ISIS 175510 (SEQ ID NO: 47) and ISIS 298697 (SEQ ID NO: 141) are targeted to human HIF-1α ASOs; ISIS 222035 (SEQ ID NO: 244) is targeted to human HIF-2α; and ISIS 129688 (TTCGCGGCTGGACGATTCAG; SEQ ID NO: 442) is an unrelated control. 10/35 is an equal mixture of ISIS 175510 and 222035 (HIF1α and HIF2α inhibitory oligonucleotides). ISIS 97/35 is an equal mixture of ISIS 298697 and ISIS 222035 (HIF1α and HIF2α inhibitory oligonucleotides).

**[0227]** The transfection medium was switched to complete growth medium (120 μl/well) 4 h after transfection. Sixty microliters of medium was removed from the well 3 h after media switch and the cells were further incubated at normoxia or hypoxia for 16-20 h.

**Table 8**
**HIF1α mRNA expression in antisense tr ated HeLa cells**
**Shown as percent inhibition relative to control oligonucleotide**

N= Normoxia (21% $O_2$)
H= Hypoxia (1% $O_2$)

| Oligonucleotide and conditions: | Normoxia or Hypoxia | Percent inhibition of HIF1α mRNA expression after treatment with oligonucleotide at concentrations shown: | | | | |
|---|---|---|---|---|---|---|
| | | 0 | 6.25 nM | 25 nM | 100nM | 200 nM |
| 129688 | N | 0 | 0 | 0 | 30 | 47 |
| 129688 | H | 1 | 1 | 10 | 30 | 57 |
| 175510 | N | 0 | 24 | 77 | 94 | 94 |
| 175510 | H | 1 | 39 | 82 | 95 | 96 |
| 298697 | N | 0 | 44 | 72 | 91 | 93 |
| 298697 | H | 3 | 30 | 75 | 92 | 93 |
| 222035 | N | 0 | 0 | 0 | 1 | 24 |
| 222035 | H | 3 | 3 | 0 | 11 | 35 |
| 10/35 | N | 0 | 33 | 82 | 94 | 94 |
| 10/35 | H | 3 | 35 | 85 | 94 | 95 |
| 97/35 | N | 0 | 16 | 66 | 84 | 85 |
| 97/35 | H | 3 | 34 | 79 | 88 | 89 |

It can be seen that the HIF1α antisense oligonucleotides ISIS 175510 and 298697 specifically inhibited HIF1α and not HIF2α. Similar results were obtained in Hep3b human hepatocellular carcinoma cells and in U87-MG human glioblastoma cells.

**Example 25**

**Antisense modulation of HIF2α mRNA expression in cancer cells (dose response)**

**[0228]** HeLa, Hep3B, or U87-MG cells were plated in 96-well plates (8-10,000/well) 16 h prior to transfection. The following antisense oligonucleotides were delivered into cells by lipofectin (3 μg/ ml per 100 nM oligonucleotide) in Opti-Mem media (Invitrogen) at the indicated concentration: ISIS 175510 (SEQ ID NO: 47) and ISIS 298697 (SEQ ID NO: 141)

are targeted to human HIF-1α ASOs; ISIS 222035 (SEQ ID NO: 244) is targeted to human HIF-2α; and ISIS 129688 (TTCGCGGCTGGACGATTCAG; SEQ ID NO: 442) is an unrelated control. 10/35 is an equal mixture of ISIS 175510 and 222035 (HIF1α and HIF2α inhibitory oligonucleotides). ISIS 97/35 is an equal mixture of ISIS 298697 and ISIS 222035 (HIF1α and HIF2α inhibitory oligonucleotides). The transfection medium was switched to complete growth medium (120 µl/well) 4 h after transfection. Sixty microliters of medium was removed from the well 3 h after media switch and the cells were further incubated at normoxia or hypoxia for 16-20 h.

**Table 9**
**HIF2α mRNA expression in ASO treated HeLa cells**
**Shown as percent inhibition relative to control oligonucleotide**

N= Normoxia (21% $O_2$)
H= Hypoxia (1% $O_2$)

| Oligonucleotide and conditions: | Normoxia or Hypoxia | Percent inhibition of HIF1α mRNA expression after treatment with oligonucleotide at concentrations shown: | | | | |
|---|---|---|---|---|---|---|
| | | 0 | 6.25 nM | 25 nM | 100nM | 200 nM |
| 129688 | N | 0 | 0 | 16 | 12 | 21 |
| 129688 | H | 0 | 0 | 4 | 12 | 50 |
| 175510 | N | 0 | 1 | 0 | 0 | 0 |
| 175510 | H | 0 | 8 | 0 | 4 | 0 |
| 298697 | N | 0 | 0 | 10 | 48 | 65 |
| 298697 | H | 0 | 0 | 11 | 52 | 58 |
| 222035 | N | 0 | 0 | 62 | 93 | 96 |
| 222035 | H | 0 | 19 | 73 | 94 | 96 |
| 10/35 | N | 0 | 0 | 77 | 96 | 96 |
| 10/35 | H | 0 | 21 | 78 | 94 | 95 |
| 97/35 | N | 0 | 0 | 63 | 89 | 95 |
| 97/35 | H | 0 | 34 | 79 | 96 | 96 |

It can be seen that the HIF2α antisense oligonucleotide ISIS 222035 specifically inhibited HIF2α relative to HIF1α. The oligonucleotide ISIS 298697, designed to target human HIF1α,

showed some ability to inhibit HIF2α expression as well. This oligonucleotide has perfect complementarity to the HIF1α target sequence and was found to have only two mismatches to the human HIF2α. Similar results were seen in U87-MG human glioblastoma cells and HepG3 hepatocellular carcinoma cells.

**Example 26**

**HIF2α plays a major role in the induction of VEGF by hypoxia in U87-MG cells**

**[0229]** Genes whose products are dramatically induced by hypoxia (or $CoCl_2$, a mimic of hypoxia) include erythropoietin (Epo), glucose transporter-1 (Glut-1), vascular endothelial growth factor (VEGF) and Phosphofructokinase-L (PFK-L). They are induced by hypoxia to varying extents in various cell lines. As shown in previous examples, VEGF expression is induced by hypoxia in U87-MG cells. The following antisense oligonucleotides were delivered into cells by lipofectin (3 μg/ ml per 100 nM oligonucleotide) in Opti-Mem media (Invitrogen) at the indicated concentration: ISIS 175510 (SEQ ID NO: 47) and ISIS 298697 (SEQ ID NO: 141) are targeted to human HIF-1α ASOs; ISIS 222035 (SEQ ID NO: 244) is targeted to human HIF-2α; and ISIS 129688 (TTCGCGGCTGGACGATTCAG; SEQ ID NO: 442) is an unrelated control. 10/35 is an equal mixture of ISIS 175510 and 222035 (HIF1α and HIF2α inhibitory oligonucleotides). ISIS 97/35 is an equal mixture of ISIS 298697 and ISIS 222035 (HIF1α and HIF2α inhibitory oligonucleotides).

**Table 10**

**HIF2α plays a major role in the induction of VEGF by hypoxia in U87-MG cells**

| Oligonucleotide and conditions: | Normoxia or | R lative VEGF mRNA expression after tr atment with oligonucleotide at concentrations shown: |
|---|---|---|

| | Hypoxia | | | | | |
|---|---|---|---|---|---|---|
| | | 0 | 6.25 nM | 25 nM | 100nM | 200 nM |
| 129688 | N | 100 | 103 | 111 | 73 | 81 |
| 129688 | H | 372 | 378 | 346 | 363 | 383 |
| 175510 | N | 100 | 86 | 65 | 61 | 62 |
| 175510 | H | 372 | 397 | 407 | 338 | 392 |
| 298697 | N | 100 | 111 | 81 | 56 | 73 |
| 298697 | H | 372 | 413 | 342 | 312 | 275 |
| 222035 | N | 100 | 94 | 69 | 48 | 45 |
| 222035 | H | 372 | 399 | 257 | 131 | 108 |
| 10/35 | N | 100 | 81 | 48 | 45 | 44 |
| 10/35 | H | 372 | 431 | 254 | 110 | 80 |
| 97/35 | N | 100 | 119 | 63 | 45 | 47 |
| 97/35 | H | 372 | 409 | 289 | 124 | 85 |

ISIS 175510, which specifically inhibits HIF1α and not HIF2α, was found to have no effect on VEGF induction by hypoxia in U87-MG cells. In contrast, ISIS 222035, which specifically inhibits HIF2α and not HIF1α, caused a dose-dependent decrease in VEGF induction. ISIS 298697, which was designed to target HIF1α but was found to have crossreactivity with HIF2α, also interfered with VEGF induction by hypoxia. Thus HIF2a plays a major role in the induction of VEGF by hypoxia in U87-MG cells.

**Example 27**

**HIF2α plays a major role in the induction of Epo by hypoxia in Hep3B cells**

**[0230]** Genes whose products are dramatically induced by hypoxia (or $CoCl_2$, a mimic of hypoxia) include Epo, Glut-1, VEGF and PFK-L. They are induced by hypoxia to varying extents in various cell lines. Epo (erythropoietin) expression is induced by hypoxia in Hep3B cells. The following antisense oligonucleotides were delivered into Hep3B cells by lipofectin (3 μg/ ml per 100 nM oligonucleotide) in Opti-Mem media (Invitrogen) at the

indicated concentration: ISIS 175510 (SEQ ID NO: 47) and ISIS 298697 (SEQ ID NO: 141) are targeted to human HIF-1α ASOs; ISIS 222035 (SEQ ID NO: 244) is targeted to human HIF-2α; and ISIS 129688 (TTCGCGGCTGGACGATTCAG; SEQ ID NO: 442) is an unrelated control. 10/35 is an equal mixture of ISIS 175510 and 222035 (HIF1α and HIF2α inhibitory oligonucleotides). ISIS 97/35 is an equal mixture of ISIS 298697 and ISIS 222035 (HIF1α and HIF2α inhibitory oligonucleotides).

**Table 11**

**HIF2α plays a major role in the induction of Epo by hypoxia in Hep3B cells**

| Oligonucleotide and conditions: | Normoxia or Hypoxia | Relative Epo mRNA expression after treatment with oligonucleotide at concentrations shown: Shown as -Fold induction over control | | | | |
|---|---|---|---|---|---|---|
| | | 0 | 6.25 nM | 25 nM | 100nM | 200 nM |
| 129688 | N | 1 | 1 | 0 | 3 | 11 |
| 129688 | H | 531 | 586 | 433 | 261 | 128 |
| 175510 | N | 1 | 8 | 3 | 3 | 2 |
| 175510 | H | 531 | 577 | 542 | 326 | 144 |
| 298697 | N | 1 | 9 | 11 | 12 | 3 |
| 298697 | H | 531 | 436 | 326 | 52 | 6 |
| 222035 | N | 1 | 3 | 3 | 2 | 1 |
| 222035 | H | 531 | 302 | 101 | 2 | 2 |
| 10/35 | N | 1 | 2 | 0 | 0 | 3 |
| 10/35 | H | 531 | 212 | 30 | 0 | 1 |
| 97/35 | N | 1 | 2 | 0 | 1 | 4 |
| 97/35 | H | 531 | 194 | 29 | 2 | 1 |

ISIS 175510, which specifically inhibits HIF1• and not HIF2•, was found to have no effect on Epo induction by hypoxia in Hep3B cells. In contrast, ISIS 222035, which specifically inhibits HIF2• and not HIF1•, caused a dose-dependent decrease in Epo induction. ISIS 298697, which was designed to target HIF1• but was found to have crossreactivity with HIF2•, also interfered with Epo induction by hypoxia. Thus HIF2a plays a major role in the induction of Epo by hypoxia in Hep3B cells.

**Example 28**

**Both HIF1α and HIF2α play a major role in the induction of VEGF by hypoxia in HeLa cells**

**[0231]** Genes whose products are dramatically induced by hypoxia (or $CoCl_2$) include Epo (erythropoietin), Glut-1, VEGF and Phosphofructokinase (PFK)-L. They are induced by hypoxia to varying extents in various cell lines. VEGF expression is induced by hypoxia in HeLa cells. The following antisense oligonucleotides were delivered into cells by lipofectin (3 μg/ ml per 100 nM oligonucleotide) in Opti-Mem media (Invitrogen) at the indicated concentration: ISIS 175510 (SEQ ID NO: 47) and ISIS 298697 (SEQ ID NO: 141) are targeted to human HIF-1α ASOs; ISIS 222035 (SEQ ID NO: 244) is targeted to human HIF-2α; and ISIS 129688 (TTCGCGGCTGGACGATTCAG; SEQ ID NO: 442) is an unrelated control. 10/35 is an equal mixture of ISIS 175510 and 222035 (HIF1• and HIF2• inhibitory oligonucleotides). ISIS 97/35 is an equal mixture of ISIS 298697 and ISIS 222035 (HIF1• and HIF2• inhibitory oligonucleotides).

**Table 12**

**HIF1α and HIF2α play a major role in the induction of VEGF by hypoxia in HeLa cells**

| Oligonucleotide and conditions: | Normoxia or Hypoxia | Relative VEGF mRNA expression after treatment with oligonucleotide at concentrations shown: | | | | |
|---|---|---|---|---|---|---|
| | | 0 | 6.25 nM | 25 nM | 100nM | 200 nM |
| 129688 | N | 100 | 119 | 100 | 85 | 93 |
| 129688 | H | 284 | 283 | 289 | 234 | 209 |
| 175510 | N | 100 | 95 | 132 | 110 | 113 |
| 175510 | H | 284 | 249 | 157 | 113 | 106 |
| 298697 | N | 100 | 84 | 105 | 93 | 93 |
| 298697 | H | 284 | 211 | 144 | 106 | 108 |
| 222035 | N | 100 | 111 | 114 | 92 | 67 |
| 222035 | H | 284 | 260 | 209 | 144 | 77 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 10/35 | N | 100 | 94 | 97 | 76 | 58 |
| 10/35 | H | 284 | 214 | 104 | 74 | 70 |
| 97/35 | N | 100 | 106 | 80 | 65 | 56 |
| 97/35 | H | 284 | 207 | 108 | 73 | 60 |

In this experiment all oligonucleotides except for the control (129688) interfered with induction of VEGF by hypoxia in HeLa cells. Thus both HIF1α and HIF2α play a major role in the induction of VEGF by hypoxia in HeLa cells. Because the relative role of HIF1α and HIF2α in hypoxic induction depends both on cell type and by induced gene (e.g., VEGF vs Epo), it is believed to be preferred to target both HIF1α and HIF2α for antisense inhibition. This may be achieved by a single cross-HIF antisense compound (such as ISIS 298697) or by a combination of one or more antisense compounds targeted to HIF1α and one or more antisense compounds targeted to HIF2α. Compounds administered in combination may be given simultaneously or sequentially.

**Example 29**

**Designing and testing HIF1•/HIF2• cross-reacting antisense compounds**

**[0232]** The human HIF1α and HIF2α target sequences were compared for regions of identity but none were found to be as long as 20 nucleotides. However, based on the somewhat limited sequence homology between the human HIF1α and HIF2α target sequences, a series of antisense sequences were designed which were perfectly complementary to either HIF1α or HIF2α and which had no more than 4 mismatches to the other HIFα. These compounds are shown in Table 13. The primary target sequence (perfect complementarity) is shown in the "target" column and the number of mismatches against the other HIF is shown in subsequent columns. "Target site" refers to position on the primary target sequence.

**Tabl 13**

**HIF1α / HIF2α crossreacting antisense sequences**

| ISISNO | OLIGO_SEQ | SEQ ID NO | Target | # Mis-match vs HIF1α | #Mis-matches vs HIF2α | Target site | HIF1α ~EC50 | HIF2α ~EC50 |
|---|---|---|---|---|---|---|---|---|
| 129688 | TTCGCGGCTGGACGATTCAG | 442 | Control | | | | | |
| 330460 | CCTCATGGTCGCAGGGATGA | 443 | HIF2α | 2 (G-A, G-U) | | 554 | | |
| 330462 | TCTCCTCATGGTCGCAGGGA | 444 | HIF2α | 3 (G-A, G-U, C-A) | | 557 | | |
| 222013 | CGAATCTCCTCATGGTCGCA | 233 | HIF2α | 4 (G-U, C-A, A-G, G-A) | | 561 | | |
| 298697 | TCCTCATGGTCACATGGATG | 141 | HIF1α | | 2 (A-C, T-C) | 673 | 5 | 30 |
| 330447 | TCATGGTCACATGGATGAGT | 445 | HIF1α | | 2 A-C, T-C) | 670 | 8 | 50 |
| 330449 | CCTCATGGTCACATGGATGA | 446 | HIF1α | | 2 A-C, T-C) | 672 | 5 | 30 |
| 330448 | CTCATGGTCACATGGATGAG | 447 | HIF1α | | 2 (A-C, T-C) | 671 | | |
| 330452 | ATTTCCTCATGGTCACATGG | 448 | HIF1α | | 3 (A-C, T-C, G-T) | 676 | | |
| 330470 | AAACCCTCCAAGGCTTTCAG | 449 | HIF2α | 2 (G-U, C-U) | | 423 | 45 | 20 |
| 326743 | TCCTCATGGTCGCAGGGATG | 450 | HIF2α | 2 G-A, G-U) | | 555 | 40 | 10 |

Thus it is possible to inhibit both HIF1α and HIF2α with a single crossreacting oligonucleotide, although the relative antisense efficacy is not equal for the two forms because of imperfect homology to one HIFα or the other.

**Example 30**

**Crossr acting HIF1α/HIF2α antisense compounds containing "universal" bases**

**[0233]** In order to try to get antisense compounds that were highly potent against both HIF1α and HIF2α targets, the nucleobases at the sites of the mismatches against one or the other HIF were replaced with the "universal bases" inosine or 3'nitro-pyrrole. Inosine has the ability to pair with G, U or C. If there was an A at the particular position of either of the sequences, we used 3-nitropyrrole. This is a base that does not have binding affinity to any of the bases, but also does not cause steric hindrance of the duplex. These oligos were screened and found to be active against both targets with an intermediate potency. This is shown in Table 14. In the table, "I" indicates inosine and "P" indicates 3-nitropyrrole.

**Table 14**

**HIF1α / HIF2α crossreacting antisense compounds containing universal bases**

| ISISNO | OLIGO_SEQ | SEQ ID NO | Target | # Mis-match vs HIF1α | #Mis-match vs HIF2α | Target site | HIF1α ~EC50 | HIF2α ~EC50 |
|---|---|---|---|---|---|---|---|---|
| 326743 | TCCTCATGGTCGCAGGGATG | 450 | HIF2α | 2 (G-A,G-U) | | 555 | 40 | 10 |
| 298697 | TCCTCATGGTCACATGGATG | 141 | HIF1α | | 2 (A-C,T-C) | 673 | 5 | 30 |
| 330449 | CCTCATGGTCACATGGATGA | 446 | HIF1α | | 2 (A-C,T-C) | 672 | 5 | 30 |
| 337223 | TCCTCATGGTCICAPGGATG | 451 | HIF1α and HIF2α | 2 (I-T,P-A) | 2 (I-C,P-C) | 673 | 25 | 15 |
| 337224 | CCTCATGGTCICAPGGATGA | 452 | HIF1α and HIF2α | 2 (I-T,P-A) | 2 (I-C,P-C) | 672 | 25 | 15 |

Introduction of universal bases into the antisense compounds at the site of mismatches resulted in a more equal inhibitory effect for both HIF1α and HIF2α.

**Example 31**

**Tube formation assay to determine effect of HIF1α and HIF2α antisense inhibitors on angiogenesis**

**[0234]** Angiogenesis is stimulated by numerous factors that promote interaction of endothelial cells with each other and with extracellular matrix molecules, resulting in the formation of capillary tubes. This process can be reproduced in tissue culture by the formation of tube-like structures by endothelial cells. Loss of tube formation *in vitro* has been correlated with the inhibition of angiogenesis *in vivo* (Carmeliet et al., (2000) Nature 407:249-257; and Zhang et al., (2002) Cancer Research 62:2034-42), which supports the use of *in vitro* tube formation as an endpoint for angiogenesis.

**[0235]** Angiogenesis, or neovascularization, is the formation of new capillaries from existing blood vessels. In adult organisms this process is typically controlled and short-lived, for example in wound repair and regeneration. However, aberrant capillary growth can occur and this uncontrolled growth plays a causal and/or supportive role in many pathologic conditions such as tumor growth and metastasis. In the context of this invention "aberrant angiogenesis" refers to unwanted or uncontrolled angiogenesis. Angiogenesis inhibitors are being evaluated for use as antitumor drugs. Other diseases and conditions associated with angiogenesis include arthritis, cardiovascular diseases, skin conditions, and aberrant wound healing. Aberrant angiogenesis can also occur in the eye, causing loss of vision. Examples of ocular conditions

involving aberrant angiogenesis include macular degeneration, diabetic retinopathy and retinopathy of prematurity.

**[0236]** The tube formation assay is performed using an *in vitro* Angiogenesis Assay Kit (Chemicon International, Temecula, CA), or growth factor reduced Matrigel (BD Biosciences, Bedford, MA). HUVECs were plated at 4000 cells/well in 96-well plates. One day later, cells were transfected with antisense and control oligonucleotides according to standard published procedures (Monia et al., (1993) J Biol Chem. 1993 Jul 5;268(19):14514-22) using 75nM oligonucleotide in lipofectin (Gibco, Grand Island, NY). Approximately fifty hours post-transfection, cells were transferred to 96-well plates coated with ECMatrix™ (Chemicon International) or growth factor depleted Matrigel. Under these conditions, untreated HUVECs form tube-like structures. After an overnight incubation at 37°C, treated and untreated cells were inspected by light microscopy. Individual wells were assigned discrete scores from 1 to 5 depending on the extent of tube formation. A score of 1 refers to a well with no tube formation while a score of 5 is given to wells where all cells are forming an extensive tubular network.

**Table 15**

**Effect of HIF1α and HIF2α antisense oligonucleotides on angiogenic tube formation**

**[0237]** ISIS 29848 (NNNNNNNNNNNNNNNNNNNN; SEQ ID NO: 453) is a control oligonucleotide containing an equal mixture of the bases A,C, G and T at every position. ISIS 298695 (SEQID NO: 139) and ISIS 298750 (Seq; SEQID NO: 193) are targeted to HIF1α; ISIS 330447 (Seq; SEQID NO: 445) is a cross-HIF oligonucleotide having perfect complementarity to HIF1α target and imperfect complementarity (and thus less

inhibitory effect) for HIF2α; ISIS 222035 (SEQ ID NO: 244) and 222025 (SEQ ID NO: 239) are targeted to HIF2α and ISIS 326743 is a cross-HIF oligonucleotide having perfect complementarity to HIF2α target and imperfect complementarity (and thus less inhibitory effect) for HIF1α.

| ISIS # | Target | 0 | 10 nM | 35 nM | 75 nM |
|---|---|---|---|---|---|
| 29848 | control | 5 | 5 | 4.75 | 4.375 |
| 298695 | HIF1α | 5 | 5 | 5 | 3.75 |
| 298750 | HIF1α | 5 | 5 | 4.75 | 3.25 |
| 330447 | HIF 1α /2α | 5 | 5 | 4.25 | 3 |
| 222035 | HIF2α | 5 | 5 | 3.75 | 1.75 |
| 222025 | HIF2α | 5 | 5 | 3.5 | 1.75 |
| 326743 | HIF2α /1α | 5 | 5 | 4.75 | 5 |

As calculated from the assigned discrete scores, it is apparent that HUVEC tube formation is inhibited by reduction of HIF2α and HIF1α, singly or in combination.

**Example 32**

**Inhibition of HIF1α expression in vivo**

**[0238]** C57Bl/6 mice are maintained on a standard rodent diet and are used as control (lean) animals. Seven-week old male C57Bl/6 mice are injected subcutaneously with oligonucleotides at a dose of 25 mg/kg two times per week for 4 weeks. Saline-injected animals serve as a control. After the treatment period, mice are sacrificed and target levels are evaluated in liver using RNA isolation and target mRNA expression level quantitation (RT-PCR) as described in other examples herein.

**[0239]** Oligonucleotides used in this experiment were ISIS 298695 (SEQ ID NO: 139), ISIS 298697 (SEQ ID NO: 141), and ISIS 298750, (SEQ ID NO: 193), all targeted to mouse HIF1• and crossreactive to human HIF1•. ISIS 141923

(CCTTCCCTGAAGGTTCCTCC; SEQ ID NO: 454) is an unrelated negative control oligonucleotide. Results are shown in Table 16.

**Table 16**

**Antisense inhibition of HIF1• expression in mouse liver by antisense to HIF1•**

| ISIS # | % inhib. of HIF1• |
|---|---|
| Saline | 0 |
| ISIS 298695 | 76 |
| ISIS 298697 | 70 |
| ISIS 298750 | 74 |
| ISIS 141923 (control) | 0 |

**[0240]** The effect of inhibiting HIF1α on levels of VEGF and GLUT1 in mouse liver was also determined. These are both hypoxia-inducible targets. Results are shown in Table 17 and 18.

**Table 17**

**Effect of Antisense inhibition of HIF1• on VEGF expression in mouse liver**

| ISIS # | % inhib. of VEGF |
|---|---|
| Saline | 0 |
| ISIS 298695 | 12 |
| ISIS 298697 | 4 |
| ISIS 298750 | 0 |
| ISIS 141923 (control) | 0 |

**Table 18**

**Effect of antisense inhibition of HIF1• on GLUT1 expression in mouse liver**

| ISIS # | % inhib. of VEGF |
|---|---|
| Saline | 0 |
| ISIS 298695 | 0 |
| ISIS 298697 | 15 |

| | |
|---|---|
| ISIS 298750 | 0 |
| ISIS 141923 (control) | 22 |

**Example 33**

**Antisense inhibition of HIF1α in a mouse model of hepatocellular carcinoma (HCC)**

**[0241]** An HCC mouse model (C57BL/6-TgN(CRP-TagSV40)60-4, Taconic, Germantown NY) for hepatocellular carcinoma was used in which transgenic male mice express SV40 T-antigen (Tag) in their livers, which leads to spontaneous development of well-differentiated hepatocellular carcinoma (HCC) carcinomas (Ruther et al., **1993**, *Oncogene* 8, 87-93). HCC mice were treated with ISIS 298695, ISIS 298697 or ISIS 298750, all targeted to HIF1• or with an unrelated control oligonucleotide. HCC and wild type mice were also treated with saline alone. Results are shown in Table 19.

**Table 19**

**Antisense inhibition of HIF1• in HCC mouse liver**

| ISIS # | SEQ ID NO | % inhib. of HIF1• |
|---|---|---|
| Saline | | 0 |
| ISIS 298695 | 139 | 43 |
| ISIS 298697 | 141 | 33 |
| ISIS 298750 | 193 | 40 |
| ISIS 141923 (control) | 454 | 11 |
| C57BL6/saline | | 43 |

The effect of HIF1• inhibition on GLUT1 expression in HCC mice was also evaluated. Results are shown in Table 20.

**Table 20**

**Effect of antisense inhibition of HIF1• on GLUT1 levels in HCC mouse liver**

| ISIS # | SEQ ID NO | % inhib. of GLUT1 |
|---|---|---|
| Saline | | 0 |

| | | |
|---|---|---|
| ISIS 298695 | 139 | 0 |
| ISIS 298697 | 141 | 0 |
| ISIS 298750 | 193 | 13 |
| ISIS 141923 (control) | 454 | 18 |
| C57BL6/saline | | 2 |

**Example 34**

**Inhibition of HIF2α expression in tumor cells by wild-type p53 under hypoxia in T47D tumor cells**

**[0242]** T47D breast adenocarcinoma cells were obtained from the American Type Culture Collection (ATCC) (Manassas, VA). Cells were cultured in Gibco DMEM High glucose media supplemented with 10% FBS. p53 is a tumor suppressor gene product which is inactive or aberrant in approximately 50% of human tumors. T47D cells are p53 null, i.e. they contain inactive mutant p53. These cells express high levels of HIF2• even in normoxic conditions. Hypoxia or $CoCl_2$ induces even higher levels of HIF2• expression. In contrast, T47D cells which have been transfected with a plasmid expressing p53, thus restoring p53 function in these cells, express extremely low levels of HIF2•, even in hypoxic conditions or in $CoCl_2$ simulation of hypoxia. This increase in HIF2• in cells with aberrant p53 is believed to be a novel observation and is believed to indicate a link between p53 and the HIF pathway.

**Example 35**

**Effects of antisense inhibition of HIF1α and/or HIF2α on cancer cell proliferation under hypoxia/glucose deprivation**

**[0243]** PC-3 human prostate cancer cells were cultured as described in previous examples. Cells were electroporated

with oligonucleotide at concentrations described below and grown for 16 hours at normoxia and 0.45 g/l glucose. The medium was then replaced with either glucose (4.5 g/l glucose) or low-glucose medium (no added glucose) and cells were then kept at hypoxia (1% $O_2$) or normoxia (21% $O_2$) for another 48 hours. The effect of antisense treatment on cell proliferation was measured. Oligonucleotides were ISIS 129688 (unrelated control), ISIS 175510 (HIF1α), ISIS 222035 (HIF2α) and ISIS 298697 (HIF1α with some crossreactivity to HIF2α). Results are shown in the tables below, one table for each culture condition.

**Tabl 21**

**Effect of HIF antisense on proliferation of PC-3 cancer c lls**

**Normoxia/Glucose**

| ISIS# | Cell proliferation as percent of saline control | | | SEQ ID NO |
|---|---|---|---|---|
| | 0 nM | 10 nM | 20nM | |
| 129688 | 100 | 103 | 103 | 442 |
| 175510 | 100 | 126 | 93 | 47 |
| 222035 | 100 | 130 | 116 | 244 |
| 298697 | 100 | 118 | 86 | 141 |

**Table 22**

**Effect of HIF antisense on proliferation of PC-3 cancer cells**

**Hypoxia/Glucose**

| ISIS# | Cell proliferation as percent of saline control | | | SEQ ID NO |
|---|---|---|---|---|
| | 0 nM | 10 nM | 20nM | |
| 129688 | 100 | 104 | 99 | 442 |
| 175510 | 100 | 113 | 105 | 47 |
| 222035 | 100 | 106 | 91 | 244 |
| 298697 | 100 | 113 | 83 | 141 |

**Table 23**

**Effect of HIF antisense on proliferation of PC-3 cancer c lls Normoxia/Low Glucose**

| | Cell proliferation as percent of saline control | | | |
|---|---|---|---|---|
| ISIS# | 0 nM | 10 nM | 20nM | SEQ ID NO |
| 129688 | 100 | 107 | 105 | 442 |
| 175510 | 100 | 96 | 89 | 47 |
| 222035 | 100 | 91 | 68 | 244 |
| 298697 | 100 | 91 | 88 | 141 |

**Table 24**

**Effect of HIF antisense on proliferation of PC-3 cancer cells Hypoxia/Low Glucose**

| | Cell proliferation as percent of saline control | | | |
|---|---|---|---|---|
| ISIS# | 0 nM | 10 nM | 20nM | SEQ ID NO |
| 129688 | 100 | 105 | 103 | 442 |
| 175510 | 100 | 90 | 85 | 47 |
| 222035 | 100 | 88 | 80 | 244 |
| 298697 | 100 | 88 | 61 | 141 |

**Example 36**

**Effect of antisense inhibitors of HIFs on human tumor cell xenografts in mice**

**[0244]** Nude mice are injected in the flank with approximately $10^6$ U87-MG human glioblastoma cells. Mice are dosed with antisense compound beginning the day after tumor inoculation and continuing every other day. Oligonucleotides

used are ISIS 129688 (unrelated control), ISIS 175510 (HIF1α), ISIS 222035 (HIF2α) and ISIS 298697 (HIF1α with some crossreactivity to HIF2α). Tumor volume is measured every few days beginning 10 days after inoculation.

**[0245]** Similar xenograft studies are performed with MDA-MB231 human breast cancer cells, which are p53-deficient. Nude mice are injected in the flank with approximately $10^6$ MDA-MB231 human breast cancer cells. Mice are dosed with antisense compound beginning the day after tumor inoculation and continuing every other day. Oligonucleotides used are ISIS 129688 (unrelated control), ISIS 175510 (HIF1α), ISIS 222035 (HIF2α) and ISIS 298697 (HIF1α with some crossreactivity to HIF2α). Tumor volume is measured every few days beginning 10 days after inoculation.

**Example 37**

**Effect of antisense inhibitors of HIFs on angiogenic conditions in the eye**

**[0246]** It is believed that antisense inhibitors of HIF2α and possibly HIF1α will be useful in treatment of angiogenic conditions, because of their effect on endothelial tube formation in an in vitro model for angiogenesis (see previous examples).

**[0247]** A pig model of ocular neovascularization, the branch retinal vein occlusion (BVO) model, is used to study ocular neovascularization. Male farm pigs (8-10 kg) are subjected to branch retinal vein occlusions (BVO) by laser treatment in both eyes. The extent of BVO is determined by indirect opthalmoscopy after a 2 week period. Intravitreous injections (10 •M) of ISIS 129688 (unrelated control), ISIS 175510 (HIF1α), ISIS 222035 (HIF2α) or ISIS 298697 (HIF1α with some crossreactivity to HIF2α) are started on the day of BVO induction and are repeated at weeks 2,6, and 10 after BVO (Right eye--vehicle, Left eye--antisense molecule). Stereo

fundus photography and fluorescein angiography are performed at baseline BVO and at weeks 1,6 and 12 following intravitreous injections to measure the neovascular response. In addition capillary gel electrophoresis analysis of the eye sections containing sclera, choroid, and the retina are performed to determine antisense concentrations, and gross and microscopic evaluations are performed to determine eye histopathology.